

# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 125396

TO: Fozia Hamud

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Thursday, June 24, 2004

Art Unit: 1647 Phone: 272-0884

**Serial Number: 10 / 015393** 

From: Jan Delaval

**Location: Biotech-Chem Library** 

**Rem 1A51** 

Phone: 272-2504

jan.delaval@uspto.gov

#### Search Notes





#### STIC-Biotech/ChemLib

125396

From:

Chan, Christina

Sent: To: Wednesday, June 23, 2004 8:23 AM Hamud, Fozia; STIC-Biotech/ChemLib

Subject:

RE: rush search

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 & 1642 (571)-272-0841 Remsen, 3E89

----Original Message-----

From:

Hamud, Fozia

Sent:

Wednesday, June 23, 2004 7:56 AM

To:

Chan, Christina

Subject:

rush search

Hi Christina, 10/015,393 is a date case that I must finsih this bi-week. Would you kindly approve this rush search. Thank you very much.

Stic,

Please search SEQ ID NOs:115 and 116 of 10/015,393 against commercial and interference data bases.

Fozia Hamud Patent Examiner Art Unit 1647

Remsen: Room 4D64 Mail box: Remsen 4C70

272-0884

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Phone:	122504
Location:	
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OM nucleic - nucleic search, using sw model

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(without alignments)

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Title:

US-10-015-393A-115
Perfect score:
1808
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Scoring table: IDENTITY_NUC
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3373863 seqs, 2124099041 residues

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Minimum DB seq length: 0
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Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

RESULT 1

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                                      The present invention relates to secreted and transmembran These proteins and the DNA encoding them may be used as hy probes, in chromosome and gene mapping and in the generatisense RNA and DNA. They may also be used used to generate transgenic animals or knockout animals which are in turn u development and screening of therapeutically useful reagen acids may also be used in gene therapy
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PRO1787 that modulate glucose or free fatty acid uptake by skeletal
muscle cells, and are useful for treating diabetes, hyper- or hypo-
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27-DEC-1999;

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23-JUN-2000;

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22-MAY-2000;

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Gao W, G
Pan J, P
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Gao W, Goddard A, Godowski PJ,
Pan J, Paoni NF, Roy MA, Smith
Williams PM, Wood WI;
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28-FEB-2001; 2001WO-US006520.
01-MAR-2001; 2001WO-US006666.
01-JUN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019692.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
04-SEP-2001; 2001US-00946374.
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Gao W, Goddard A, Godowski PJ,
Pan J, Paoni NF, Roy MA, Smith
Williams PM, Wood WI;
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99WO-US02813.3.
99WO-US028551.
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2000WO-US00376.
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The invention relates to an isolated PRO polypeptide (secreted or transmembrane protein) having at least 80% amino acid sequence identity to an amino acid sequence chosen from 123 fully defined sequences as convention acid sequence signal peptides. Also include are the nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a vector comprising the vector, producing PRO, a chimaeric molecule comprising PRO fused to a heterologous amino acid sequence, and an antiport of suseful as molecular weight markers for protein PRO antibody. Pro is useful as molecular weight markers for protein cletrophoresis and also for chromosome identification. PRO is also useful for tissue typing. PRO and PRO NA are useful as hybridisation brobes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is useful in development and screening useful reagents. PRO NA is also useful for treating cancerous tumours. PRO1303 polypeptides are useful for treating cancerous tumours. PRO1248 and PRO1410 polypeptide is useful for treating candience propried is useful for treating canciency for science prolypeptide is useful for treating canciency prolypeptide are useful for stimulating calcium flux in human complical vein endothelial cells. PRO1265, PRO1250 and PRO1474 umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474
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Hillan KJ;
Watanabe CK;
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Gurney AL,
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V, Stewart TA,
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Gao W, Goddard A, Godowski PJ,
Pan J, Paoni NF, Roy MA, Smith
Williams PM, Wood WI;
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(e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418 polypeptides are useful for treating diabetes in skeletal muscle cells and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for treating Berger disease or other nephropathies associated with Schonlein-Henoch purpura, coeliac disease, dermatitis, herpetiformis or Crohn's disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418, PRO1410 and PRO1575 are useful in treating thalassaemias. The present sequence encodes a PRO protein of the invention.
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Pred. No. 0;
Mismatches useful , wound , 115; 556pp; English Baker KP, Botstein D, Desnoyers L, Gao W, Goddard A, Godowski PJ, Gr Pan J, Paoni NF, Roy MA, Smith V, Williams PM, Wood WI; Novel isolated PRO polypeptide, teardiac insufficiency disorders, thalassemias. Query Match Best Local Similarity 100.0%; Matches 1808; Conservative ( WPI; 2003-787000/74 P-PSDB; ADD38275. 2; SEQ ID NO 121 301 61 61 301 361 421 481 481 541 601 661 661 721 181 181 241 241 361 421 541 601 121 Claim D D g d g δ D <del>Q</del>  $\overset{\circ}{\circ}$ g δ d d d 장 ö ਨੋ Б à d 슝 à  $\delta$  $\delta$ ઠ

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Hillan KJ;
Watanabe CK;
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Gurney AL,
A, Tumas D,
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V, Stewart TA
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Pred. No. 0;
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Gao W, Goddard A, Godowski PJ,
Pan J, Paoni NF, Roy MA, Smith
Williams PM, Wood WI;
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Best Local Similarity 100.0%;
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betes; skeletal muscle cells; obesity;
schonlein-Henoch purpura; coeliac disease;
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Gurney AL,
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cancerous tumors, (
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Grimaldi JC,
7, Stewart T
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1808; Conservative 0; Mismatches
                                                                                                                      New isolated PRO polypeptide such as PRC PRO1244, PRO1246, useful for treating cainsufficiency disorders, wound healing,
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                                                               Baker KP, Botstein D, Desnoyers
Gao W, Goddard A, Godowski PJ,
Pan J, Paoni NF, Roy MA, Smith
Williams PM, Wood WI;
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2001WO-US006666.
2001WO-US017800.
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                                                  (GETH ) GENENTECH INC
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SDB; ADD38754.
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                                        CCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTCTGTGCAC
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Hillan KJ;
Watanabe
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Gao W, Goddard A, Godowski PJ,
Pan J, Paoni NF, Roy MA, Smith
Williams PM, Wood WI;
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02-JUN-2000; 2000WO-US015264.
23-AUG-2000; 2000WO-US023522.
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08-NOV-2000; 2000WO-US030952.
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01-DEC-2000; 2000WO-US032678.
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01-JUN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019692.
29-JUN-2001; 2001WO-US01966.
09-JUL-2001; 2001WO-US021735.
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P-PSDB; ADE50406.
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Fong S;
Hillan KJ;
Watanabe CK;
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Gurney AL,
A, Tumas D,
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Grimaldi JC,
V, Stewart TA
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Gao W, Goddard A, Godowski PJ,
Pan J, Paoni NF, Roy MA, Smith
Williams PM, Wood WI;
17-NOV-1998; 98US-0108775P.
17-NOV-1998; 98US-0108779P.
17-NOV-1998; 98US-0108779P.
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11-REB-2000; 2000WO-US000884.
11-REB-2000; 2000WO-US003865.
10-MAY-2000; 2000WO-US003865.
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                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E (bases 1 to 1808)

Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P.

The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)

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Clark, H.F.

Direct Submission

Submitted (01-AUG-2003) Department of Bioinformatics,

Inc., 1 DNA Way, South San Francisco, CA 94080, USA

Location/Qualifiers
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Matches 1808; Conservative 0; Mismatches
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82. .1077
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Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T.,
Hayashi,K.
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HELIX RESEARCH INSTITUTE
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                     CCGCAGCTTCCTGGCACTACCTGAGCCGGGAGACCCAGGACTGGCGGCCCCAGCAGACTGGCGGCCCCCAGCACTCCTGGCACTACCTGAGCCGGGAGACCCAGGAACTGGCGGCCCA
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L Chases I to 1878)

S Isogai, T. and Yamamoto, J.

Direct Submission

L Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

C E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass sequencing, clone selection and full insert sequencing: Helix Research Institute (supported by Japan Key Technology Center etc.); cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center. /protein\_id="BAC11591.1"
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AEELADVSGKYFDGLKQKAPAPEAEDEEVARRLWAESARLVGLEAPSVREQPLPR" -SEP-2002 180 130 240 190 250 310 9 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NT2 neuronal (RA) GTAGCAGGCGCCGCCGTGCTGCTCAAGGACTATGTCACCGGTGGGGCTTGCCCCAAG GCCACCATCCTGGGAAGACGGTCATCGTGACGGCCCCAACACAGGCATCGGGAAGCAG GTAGCAGGCGCCCCGTGCTGCTCAAGGACTATGTCACCGGTGGGGCTTGCCCCAGCAAG PRI 03-weakly .. 0 Length 1878 acid /cione\_ilD=\_Mizkr2...
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/note="unnamed protein product" mRNA linear ne NT2RP2004966 Indel 10, sednence) DB 9; 1. 1878 /organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606" /clone="NT2RP2004966" /cell\_line="NT2" /cell\_type="teratocarcinoma" /clone\_lib="NT2RP2" clone Mismatches 99.1%; Score 1792; larity 99.4%; Pred. No. 0; Conservative 0; Mismatche AK075392
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Strausberg, R. Direct Submission  Unscit Submission  Submitted (02-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  NIH-MGC Project URL: http://mgc.nci.nih.gov  On Aug 19, 2003 this sequence version replaced gi:14602729.  Contact: MGC help desk  Email: cgapbs-r@mail.nih.gov  Tissue Procurement: ATCC  CDNA Library Preparation: Rubin Laboratory  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  DNA Sequencing by: Institute for Systems Biology  http://www.systemsbiology.org  contact: amadan@systemsbiology.org  Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha  Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting	C C C C C C C C C C C C C C C C C C C	/note="Vector: p 12006 /gene="RDH13" /db_xref="Locus] 4751257 /codon_start=1 /product="retinc /protein_id="AAF /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="di:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="di:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:146 /db_xref="Gi:	/db_xref="CDD:pfam00106"  Match ocal Similarity 99.7%; Pred. No. 1.9e-301; s 1661; Conservative 0; Mismatches 4; 1  144 CAAGGACTATGTCACGGTGGGCTTGCCCCAGCAAGGCCAG 323 CAGGGACTATGTCACGGTGGGCTTGCCCCAGCAAGGCCAG  [
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TCCCACCTTCCTATCAATTCTCATGGTAGTCC 1779
                         GCACGCCATGGAGTGGGAACCCCACCAGCTGC 1719
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CTTCCTGTGCCAGAGCCCAGAGAGCAGG 2887
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Pred. No. 7.2e-215;
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Patent: WO 014446-A 6 21-JUN-2001
Millennium Pharmaceuticals, Inc. (
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21612, 21615, 21620, 21676, 33756, novel human alcohol
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
sıze: 204523; sum-of-contigs
coverage: 6.54 in Q20 bases; agarose-fp
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Homo sapiens chromosome 19 clone RP11-700B5, WORKING DRAFT
AC019238
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HTG; HTGS PHASE1; HTGS DRAFT.
Homo sapiens (human)
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Waterston, R.H.
The sequence of Homo sapiens clone Unpublished 2 (bases 1 to 204340)
Waterston, R.H.
Direct Submission
Submitted (30-DEC-1999) Genome Sequencing Center, W.
University School of Medicine, 4444 Forest Park Park MO 63108, USA
On Aug 17, 2000 this sequence version replaced gi:9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGAGCCGGCGGCTGCAAGGCTCTGGTGACTGTCAACGCCCTGCACC
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Length 204340;
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apiens chromosome 19 clone CTC-550B14, complete 5 (76.8 di:2267569)  appiens (human) appiens (	147996 CTGGCCGTGGCGAG 961 AAGGCCCCGGCCCCC 147936 AAGGCCCCGGCCCCC 1021 GCCCGCCTGGTGGGC 147876 GCCCGCCTGGTGGGC
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Secretory protein or membrane protein
FH Key Location/Qualifiers
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Location/Qualifiers

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JP 2002017376-A/387
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07-JUL-2000 JP 2000253173
TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI SUGIYAMA,
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Homo sapiens
Gutaryota; Metazoa; Chordata; Craniata; Verteinamalia; Eutheria; Primates; Catarrhini; Hom

I (bases 1 to 554)
Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sur Hayashi, K.
Secretory protein or membrane protein
Patent: JP 2002017376-A 387 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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PN JP 2002017376-A/387
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253173
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PI KOJI HAYASHI
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Ota,T., Isogai,T., Nishikawa,T., Kawai,Y.,
Hayashi,K.
Secretory protein or membrane protein
Patent: EP 1067182-A 560 10-JAN-2001;
Helix Research Institute (JP)
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BX393531.1 GI:30627901

SMMmalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 9526.r. Contac

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Invitrogen. This sequence belongs to sequence cluster 9526.r. Contac

Cgi-bin/cluster.cgi?seq=CSODB006AH11QP1&cluster=9526.r. Contac

Feng Liang Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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1. 896
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IMAGE:6597198 5', mRNA sequence.
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Homo sapiens

Homo sap
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Pred. No. 6e-165;
0; Mismatches 7;
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   lay Avenue Genoscope sequence ID : CSODBOO6AH11QP1.

Location/Qualifiers
1. .1201
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/db_xref="taxon:9606"
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/clone lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
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Pred. No. 6.3e-179;
7; Mismatches 30;
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Best Local Similarity 95.9%;
Matches 1006; Conservative
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OMMENT Contact: Robert Strausberg, Ph.D.  Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP  cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Co  Clone distribution: MGC clone distribution found through the I.M.A.G.E. Consortium/LLN  http://image.llnl.gov  Plate: LLCM2380 row: d column: 04  High quality sequence stop: 717.  High quality sequence stop: 717.  Appering Location/Qualifiers  /organism="Homo sapiens" // Appering Laxon:9606" // Lissue type="mRNA" // Lissue type="melanoma, riskue type="melanoma, riskue") // Lissue type="melanotic melanoma, riskue type="melanoma, riskue type="melanoma, riskue type="melanoma, riskue") // Lissue type="melanotic melanoma, riskue type="melanoma, riskue type="melanoma, riskue")	lab host="DH10B (phage-resistant)"  lote="Organ: skin; Vector: pOTB7; Site 1:  lote="Organ: skin; Vector: pOTB7; Site 1:  lote="Organ: skin; Vector: pOTB7; Site 1:  lote ECORI/XhoI sites using the following  loto ECORI/XhoI sites using by Ling  loto Ecority of Gerald M. Rubin (University  loto Gerald M. Rubin (University  loto Gerald M. Rubin (University  loto Library."  loto Li	######################################	121 ĠĊĀĠĠĊĠĊĠĊĠĊĠĊĠĊĠĊĠĊĠĊĊĀĀĠĠĀĊŢĀŢĠŢĊĀĊ 184 ACCATCCCTGGGAAGACGGTCATCGTGACGGCGC 	364 CACCTGGACTTGCTTCCTCAAGTCTATCGAGAGTTTGCAGCAAAGATCATTGAAGA 42
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Homo sapiens (human)

Homo sapiens

Homo sapiens

Homo sapiens

Bukaryoca, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryoca, Wetazoa; Chordata; Catarrini; Hominidae; Homo.

I (bases 1 to 935)

NIH-MGC http://mgc.nci.nih.gov/.

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Connect: Robert Strausberg, Ph.D.

Email: Gapbs-remail.nih.gov

Tissue Procurement: DcTD/DTP

CDNA Library Arzayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://ingel.lln.gov

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://ingel.lln.gov

Clone distribution aspiens:

http://ingel.lln.gov

Plate: LLCM2432 row: I column: 08

High quality sequence stop: 657.

Location/Qualifiers

L. 355

/organism: Homo sapiens:

// Alb. hogf="MRNM" MGC_112"

// Clone=llne" MRNM made by oligo-dT priming Directionally cloned into EcoRI/KhOI sites using the following 5' adaptor:

// Alb. hogf="MRNM" MRN" Wactor: poTB7; Site 1: XhoI; Site 2:

// Alb. hogf="MRNM" MRN" Wactor: poTB7; Site 1: XhoI; Site 2:

// Alb. hogf="MRNM" MRN" Wactor: poTB7; Site 1: XhoI; Site 2:

// Alb. hogf="MRNM" MRN" Wactor: poTB7; Site 1: XhoI; Site 2:

// Alb. hogf="MRNM" MRN" Wactor: poTB7; Site 1: XhoI; Site 2:

// Alb. hogf="MRNM" MRN" Wactor: poTB7; Site 1: XhoI; Site 2: Adaptor:

GGCACAGG(6). Library constructed by Ling Hong in the following 5' adaptor:

Berkeley, using SAP-CDNA synthesis kit California,

Berkeley, using SAP-CDNA synthesis kit decades

NIH_MCC Library."

NIH_MCC Library."
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Query Match

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BM810961
AGENCOURT_6587923 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5473329
5', mRNA sequence.
BM810961
BM810961.1 GI:19127784
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Home sapiens (human)

Home sapiens (human)

Home sapiens

Home sapiens

Budaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Budaryota; Metazoa; Chordata; Cararrhini; Hominidae; Home.

Budaryota; Metazoa; Chordata; Cararrhini; Hominidae; Home.

I (bases 1 to 88)

NIH-MGC http://mgc.nci.nih.gov/.

Mational Institutes of Health, Mammalian Gene Collection, (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nigov

Tissue Precorement. ATC.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: NIH Intramural Sequencing Center

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1731 row: n column: 18

High quality sequence stop: 811.

Location/Qualifiers

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/ Corganism-Home sapiens"

/ Ab xref="rema" Home sapiens"

/ Ab xref="rema" Home sapiens"

/ Ab xref="rema" Home sapiens"

/ Lissue type="mRMN"

/ Ab xref="rema" Colon; Vector: porB7; Site 1: Xho1; Site 2:

/ Conse: INAGE: 486 2013.

/ Library Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of california, Berkeley) using ZAP-CDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)"
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9 778 96 316 136 718 838 8 9 8 196 958 256 1018 1078 ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT VERSION KEYWORDS SOURCE FEATURES Q D d ð da අ d g  $\delta$ ò  $\dot{\circ}$ ઠે ठ 739 799 620 680 721 781 382 441 421 501 481 561 601 661 202 241 301 61 SCTGCTGGACAG CCCATGTTGCTGG SCGAGIGGACAIT CCGCCGTGCTGC CTGCCAGAGCAAGCTCGCCATCGTCCTCTTCACCAAGGAGCTGAGCCGGCGGC-TGCAAG GCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGTCCCCGGCCCGGCAAGCTCCCCGGCCCGGCCCGGCCCGGCCCGGCCCGGCCCGGCCCGGCCCGGCCCGGCCCGGCCCGGCCAAGCTCCGGCCCGGACGCCTGACGCCTGACGCCTGTCCCCGGCCCGGCC .. 9 882 linear I GAGGAGGCAACATCATCCTGGCCTGCCGAGACATGGAGAAGTGTGAGGC Length 8 9 5 8 8 0 mRNA sapiens Score 791.4; DB 12; Pred. No. 2.6e-146; 0; Mismatches 16; AGENCOURT 6607565 NIH MGC 41 Homo 5', mRNA sequence.
BM914938 43.8%; 97.5%; vative Similarity 7; Conserv S 7. 740 722 Query Match Best Local S Matches 857 (1) 82 482 542 681 857 2 23 323 362 502 562 662 83 143 122 203 242 302 383 422 182 263 442 RESULT 7 BM914938 LOCUS ORIGIN d 유 ö 슝 g 셤 d Б ö q D δ d à Б  $\stackrel{\sim}{\circ}$ à à à  $\stackrel{\sim}{\circ}$  $\delta$ 

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Best Local Similarity 95.0%; Pred. No. 2.1e-143;
Matches 814; Conservative 0; Mismatches 40;
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laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:6672291"
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/tissue_type="teratocarcinoma, cell line"
/lab_host="DH10B (phage_resistant)"
/clone_lib="NIH_MGC_109"
/note="Organ: ovary; Vector: pOTB7; Site_l: EcoRI; Site_2:
Xhol; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/Xhol sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
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Homo sapiens (human)

Homo sapiens Eutheria; Primates; Craniata; Vertebrata; Bute Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Hom ammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom 1 (bases 1 to 892)

National Institutes of Health, Mammalian Gene Collection Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM2952 row: j column: 03

High quality sequence stop: 617.

Location/Qualifiers

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Sylogon NIH_MGC_112 Homo sapiens CDNA clone INAGE:6110921
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NA GENCOURT_7984090 NIH_MGC_112 Homo sapiens CDNA clone INAGE:6110921
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BU190625.1 GI:22704609
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ECORI; cDNA made by oligo-dT priming. Direction of Ecori/Xhoi sites using the following 5 GGCACGAG(G). Library constructed by Ling Holaboratory of Gerald M. Rubin (University of Berkeley) using ZAP-cDNA synthesis kit (Stra Superscript II RT (Life Technologies). Note NIH_MGC Library."
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Pred. No. 3.4e-136;
); Mismatches 16;
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/do xref="taxon:9606"
/clone="IMAGE:5016556"
/tissue type="small cell carcinoma"
/cell line="MGC3"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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            Homo sapiens (human)

SM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1019)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Inpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP

CONA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM1827 row: e column: 05

High quality sequence stop: 755.

Location/Qualifiers

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I. .1019
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1019 bp Homo sapiens

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The Frantom Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

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Adachi, J. Alzawa, K. Akimura, T., Arakawa, T., Bonc, H., Carninci, P., Rukuda, S., Furunco, M., Hanagaki, T., Hara, A., Hashizume, W., Harakashida, S., Furunca, M., Hanagaki, T., Harakashida, T., Hayashida, X., Hayashida, X., Hayashida, Y., Kojima, Y., Konda, M., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Muyazaki, R., Ohno, M., Ohsato, N., Katoh, H., Satoki, K., Saitoh, H., Satoki, S., Saitoh, H., Satoki, S., Saitoh, H., Satoki, M., Satoki, M., Sakaki, K., Sakazi, M., Sakazi, C., Sakazi, K., Sakazi, M., Sakazi, C., Sakazi, K., Sakazi, M., Sakazi, C., Sakazi, M., Sakazi, M., Sakazi, C., Sakazi, M., Sakazi, M.,
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weakly similar to SD07613P [Drosophila melanogaster]
(SPTR|Q960C7, evidence: FASTY, 53.6%ID, 95.7%length,
match=948)"
                                                                                                                                                                                      Team and
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 11076861
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Functional annotation
Nature 409, 685-690 (2
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                                                                                                                                                        TAAACTGGGAATGGCCGAGGAGAA-GGGGCTCTGTGCACTTGCAGGCCACGTCAGGAGAGAGAGGAGATGCTGGGAATGGCCGAGGAGGAAGGGGGCTCCGTGCACTTGCCGGCCACGTCAGGAGA
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Mus musculus 14 days embryo liver cDNA, RIKEN full-leng library, clone:4432411109 product:weakly similar to SD(E) forsophila melanogaster], full insert sequence.

AKO28434

AKO28434.1 GI:26324391

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euthammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu
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High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 9565
Fax: 319 335 9565
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
Location/Qualifiers
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Hammalia; Eutheria; Primates; Catarrhini; Hominidae; Honandlo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facil discovery
Genome Res. 6 (9), 791-806 (1996)
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/dev stage="fetal and adult"
/dev stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (Tl phage resistant)"
/clone lib="UI-E-EJU"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJO is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes,
AGAATCAAGA; lens, CGATTAGGGA; eye anterior segment,
AATGCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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/clone="UI-B-EJO-aio-b-02-0-UI"
/tissue_type="fetal eyes, lens, eye an optic nerve, retina, Retina Foveal and choroid"
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imbrane bound protein; receptor; immunoadhesion; pharmaceutical; ID NO:116 sequence SEQ acid membrane 331 98US-0098716P. 98US-0098749P. 98US-0098821P. 98US-00998821P. 98US-0099536P. 98US-0099536P. 98US-0099598P. 98US-0099598P. 98US-0099598P. 98US-0099741P. 98US-0099741P. 98US-0099741P. 98US-0099741P. 98US-0099763P. 98US-0099815P. 98US-0099815P. 98US-0100388P. 98US-0100388P. 98US-0100388P. 98US-0100388P. 98US-0100388P. amino entry) Human; PRO polypeptide; mtransmembrane; secretion; (UNQ736) (first standard; WO200012708-A2 PRO1430 sapiens. 01-SEP-1998; 01-SEP-1998; 02-SEP-1998; 02-SEP-1998; 02-SEP-1998; 09-SEP-1998; 09-SEP-1998; 09-SEP-1998; 10-SEP-1998; 10-SEP-1998; 10-SEP-1998; 10-SEP-1998; 10-SEP-1998; 10-SEP-1998; 10-SEP-1998; 10-SEP-1998; 16-SEP-1998; 09-MAR-2000 01-SEP-1999 08-AUG-2000 RESULT 1 AAY99372 ID AAY99372 AAY99372 Нишап Ношо 

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receptor or secreted peptide or small interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCI primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention
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Human; drug metabolising enzyme; DME-5; immunosuppressive; gene therapy; cytostatic; autoimmune disorder; inflammatory disorder; atherosclerosis; osteoporosis; eye disorder; hepatic tumour; Addison's disease; cretinism; rheumatoid arthritis; acquired immune deficiency syndrome; AIDS; anaemia; developmental disorder; endocrine disorder; iritis; acromegaly; epilepsy; thyrotoxicosis; pancreatic disorder; diabetes mellitus; obesity; adenoma; gastrointestinal disorder; nodular hyperplasia; conjunctivitis; glaucoma; actinic keratosis; metabolic disorder; dysphagia; anorexia; carcinoma; cell proliferative disorder.
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Human DME and its nucleic acid molecule are useful for
treatment and prevention of disorders associated with i
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Yao MG,
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zimzai Y,
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Yue H, Azimzai
P Bandman C
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/note=
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Hillman JL,
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Ring HZ, H
Nguyen DB,
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Hillan KJ;
Watanabe
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Gurney AL,
A, Tumas I
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Grimaldi CJ, G
V, Stewart TA,
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    gene therapy
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Gao W, Goddard A, Godowski PJ,
Pan J, Paoni NF, Roy MA, Smith
Williams PM, Wood WI;
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99US-0144758P.
99US-0145698P.
99WO-US020111.
99WO-US028313.
99WO-US028313.
99WO-US030095.
2000WO-US000219.
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                                                                                   standard; protein;
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nes 331; Conser
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20-JUL-1999;
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decreased expression of DME. Examples of such disorders include, autoimmune/inflammatory disorder such as acquired immune deficiency syndrome (AIDS), rheumatorid arthritis, osteoporosis; cell proliferative disorder such as actinic keratosis, atherosclerosis; developmental disorder such as actinic keratosis; andocrine disorder such as acromegaly, cretinism, thyrotoxicosis; pancreatic disorder such as acromegaly, cretinism, thyrotoxicosis; pancreatic disorder such as acromegaly, cretinism, thyrotoxicosis; pancreatic disorder such as disorder such as anorexia, dysphagia and hepatic tumours including metabolic disorder such as anorexia, dysphagia and hepatic tumours including disorder such as anorexia, dysphagia and hepatic tumours including nodular hyperplasia, adenomas and carcinomas. DME DNA is useful for creating 'knockin' humanised animals (pigs) or transgenic animals (mice or rats) to model human disease. DME DNA is also in useful is gene therapy. DME and its immunogenic fragments are useful for screening therapys of compounds in several drug screening assays
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Human; secreted protein; hyperproliferative disorder; multiple myeloma; haeman disorder; acquired immune deficiency syndrome; arthritis; haematopoietic disorder; systemic lupus erythematosus; atherosclerosis; reproductive system disorder; musculoskeletal disorder; renal disorder; cardiovascular disorder; neurofibromatosis; Alzheimer's disease; asthma; neurological disorder; Parkinson's disease; respiratory disorder; AIDS; emphysema; bronchitis; endocrine disorder; genetic disorder; psoriasis; inflammation; congestive heart failure; multiple sclerosis; arrhythmia; hypertension; urolithiasis; amenorrhoea; epididymitis; anaemia; allergy; gout; hepatitis; digestive disease; diabetes; goitre; infection; wound;
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                                  standard; protein;
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protein genes and AAE37272-AAE37295 represent the proteins they encode.

AAE37296-AAE37299 represent human secreted proteins they encode.

AAE37296-AAE37299 represent human secreted protein fragments. The genes and their corresponding proteins are useful in diagnosing, preventing or treating diseases or conditions such as hyperproliferative disorders (e.g. cancer), immune/haematopoietic disorders (e.g. anaemia, multiple myeloma, arthritis, asthma, acquired immune deficiency syndrome (AIDS), rheumatoid arthritis, inflammation, psoriasis, diabetes, systemic lupus erythematosus or allergy), reproductive system disorders (e.g. amenorrhoea or epididymitis), musculoskeletal disorders (e.g. gout or multiple sclerosis), cardiovascular disorders (e.g. arrhythmia, congestive heart failure, hypertension or atherosclerosis), genetic disorders (e.g. neurolighical disorders (e.g. Alzheimer's disease or Parkinson's disease), respiratory disorders (e.g. alphysema or bronchitis), endocrine disease), infections or wounds. Polynucleotides of the invention may also be used for chromosome mapping or drug screening. They are also useful in gene therappy. The present sequence represents a human secreted protein of the
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infections
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N-PSDB; AAD56357.
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98US-010254PP.
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98US-0105693PP.
98US-0106033PP.
  Human; secreted and transmembrane protein; PRO; angiogenesis; endothelial cell proliferation; wound healing; immune response; T-lymphocytes proliferation; neonatal heart hypertrophy; tumour; cardiac insufficiency disorder; calcium flux; inflammation; vascular endothelial growth factor-stimulated proliferation; mammalian kidney mesangial cell proliferation; Berger disease; nephropathy; Schanlein-Henoch purpura; celiac disease; Crohn's disease; dermatitis herpetiformis; diabetes; haemoglobin switch; insulinaemia; pancreatic beta-cell precursor cell differentiation; thalassemias; obesity; auditory hair cell regeneration; hearing loss; bone disorder; cartilage disorder; sports injury; arthritis.
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Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating various cardiac insufficiency disorders, bone and/or cartilage disorders such as sports injuries arthritis. Ferrara N, Gurney AL, TA, L, Eaton DL, Grimaldi JC, V, Stewart TA Baker KP, Botstein D, Desnoyers Gao W, Goddard A, Godowski PJ, Pan J, Paoni NF, Roy MA, Smith Williams PM, Wood WI; 03-NOV-1998; 98US-0106919P.
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20-JUN-2000; 2000WO-US001806.
20-JUN-2000; 2000WO-US001806.
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20-JUN-2001; 2000WO-US01806.
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Fong S; Hillan KJ; Watanabe C

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                                                                                                                                                                                                                                                                                                                   GKOTAL
                                                                                        e.g. PRO1491 and PRO1571, useful treating a condition responsive tagents e.g. vaccines.
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                                                                                      Novel isolated PRO polypeptides preparation of a medicament for polypeptide, and as therapeutic
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Matches 331; Conservative (
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genetic disorder.
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N-PSDB; ACD67967.
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Grimaldi JC, Gu
V, Stewart TA,
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Godowski PJ, G
Roy MA, Smith
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Goddard A, (
Paoni NF, Re
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Watanabe CK;
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                                                                                                                                                                                                       Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful preparation of a medicament for treating a condition responsive t polypeptide, and as therapeutic agents e.g. vaccines.
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Best Local Similarity 100.0%; Pred. No. 1e-165;
Matches 331; Conservative 0; Mismatches 0; Indels
                                                                                              Baker KP, Botstein D, Desnoyers L, Eaton DL, Gao W, Goddard A, Godowski PJ, Grimaldi JC, G Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Williams PM, Wood WI;
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2001WO-US021066.
2001WO-US021735.
2001US-00946374.
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20-JUN-2001;
29-JUN-2001;
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                                                                                           Baker KP,
Gao W, (
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08-00CT-119988;
08-00CT-119988;
03-00CT-119988;
03-00CT-119998;
03-00CT-119998
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Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555, PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle cells and are useful for treating diabetes or hyper- or hypo-insulinemia.
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Hillan KJ;
Watanabe (
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Gurney AL,
A, Tumas D,
                                                                                                                                                                                                                                                                                                                                                                        Length
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Grimaldi JC, Gu
V, Stewart TA,
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Best Local Similarity 100.0%; Pred. No. 1e-165;
Matches 331; Conservative 0; Mismatches 0;
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Gao W, Goddard A, Godowski PJ,
Pan J, Paoni NF, Roy MA, Smith
Williams PM, Wood WI;
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2000WO-US003565.

2000WO-US004342.

2000WO-US005841.

2000WO-US005884.

2000WO-US013705.

2000WO-US013705.

2000WO-US0137264.

2000WO-US013522.

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2000WO-US023522.

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N-PSDB; ADD70630.
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17-MAY-2000;

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22-MAY-2000;

23-MAY-2000;

24-AUG-2000;

24-AUG-2000;

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24-AUG-2000;

26-NOV-2000;

27-MAR-2001;

29-UUN-2001;

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The invention relates to an isolated PRO polypeptide (secreted or transmembrane protein) having at least 80% amino acid sequence identity to an amino acid sequence chosen from 123 fully defined sequences as given in the specification (including their extracellular domains either or without their associated signal peptides. Also include are the nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a
                                                                                       disorder;
; obesity;
eliac disease;
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Hillan KJ;
Watanabe C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    r treating
itus, hyper
                                                                  Human; secreted protein; transmembrane protein; PRO; tumour; immune response; cardiac insufficiency disorder; calcium flux; umbilical vein endothelial cell; bone disorder; cartilage disorarthritis; wound healing; diabetes; skeletal muscle cells; obes Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac dermatitis; herpetiformis; Crohn's disease; thalassaemia.
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Gurney AL,
A, Tumas I
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Grimaldi JC, (
V, Stewart TA
                                              PR0143
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                                              secreted/transmembrane protein
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Goddard A, Godowski PJ,
Paoni NF, Roy MA, Smith
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99WO-US020111.

99WO-US028313.

99WO-US028313.

99WO-US028551.

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2000WO-US00376.

2000WO-US00376.

2000WO-US003565.

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2000WO-US013705.

2000WO-US013692.

2000WO-US030873.

2000WO-US030873.

2000WO-US0308666.

2001WO-US0308666.

2001WO-US019692.

2001WO-US0136374.
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WI;
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N-PSDB; ADD39707.
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s PM, Woo
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15-SEP-1999;
30-NOV-1999;
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05-JAN-2000;
16-DEC-1999;
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17-MAR-2000;
17-MAY-2000;
17-MAY-2000;
22-MAY-2000;
22-MAY-2000;
22-MAY-2000;
23-AUG-2000;
02-JUN-2000;
01-DEC-2000;
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01-DEC-2000;
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host cell comprising the vector, producing PRO, a chimaeric molecule comprising PRO fused to a heterologous amino acid sequence, and an anti-PRO antibody. Pro is useful as molecular weight markers for protein clectrophoresis and also for chromosome identification. PRO is also useful for tissue typing. PRO and PRO MA are useful as hybridisation probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is useful in development and screening useful reagents. PRO NA is also useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1416 polypeptides are useful for treating cardiac insulficiency disorders. PRO1266 polypeptide are useful for treating cardiac insulficiency disorders. PRO1266 polypeptide are useful for treating calcium flux in human umbilical vein endothelial cells. PRO1265, PRO1250 and PRO146 polypeptides are useful for treating calcium flux in human umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1418 to 1ypeptides are useful for treating diabetes in skeletal muscle cells and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for treating diabetes in skeletal muscle cells and obesity. PRO1265, PRO1264 and PRO1382 polypeptides are useful for treating diabetes are useful for treating diabetes in skeletal muscle cells and obesity. PRO1265, PRO1264 and PRO1382 polypeptides are useful for treating diabetes in skeletal muscle cells and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for treating diabetes in skeletal muscle cells and obesity. PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418, PRO1418, PRO1275 are useful in treating that assamias. The present sequence represents a PRO protein of the invention.
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Pred. No. 1e-165;
0; Mismatches 0;
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08-0CT-1998;
   98US-0098716P.
98US-0098723P.
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Human; secreted protein; transmembrane protein; PRO; tumour; immune response; cardiac insufficiency disorder; calcium flux; umbilical vein endothelial cell; bone disorder; cartilage disorder; arthritis; wound healing; diabetes; skeletal muscle cells; obesity. Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac diseatitis; herpetiformis; Crohn's disease; thalassaemia.
                                    protein PRO1430
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98US-0098863P.
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10 - SSEP-19998;

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                    15-JAN-2004
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in protein
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Hillan
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Gurney AL,
A, Tumas D
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markers
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Grimaldi JC, Gu
.V, Stewart TA,
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Pred. No. 1e-165;
Mismatches 0
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Gao W, Goddard A, Godowski PJ,
Pan J, Paoni NF, Roy MA, Smith
Williams PM, Wood WI;
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2000WO-US003565.
2000WO-US004342.
2000WO-US005841.
2000WO-US005841.
2000WO-US013705.
2000WO-US013705.
2000WO-US014941.
2000WO-US014941.
2000WO-US013522.
2000WO-US015264.
2000WO-US023522.
2000WO-US023522.
2000WO-US023522.
2000WO-US023522.
2001WO-US023520.
2001WO-US023520.
2001WO-US036666.
2001WO-US017800.
2001WO-US017800.
2001WO-US017800.
2001WO-US01785.
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Best Local Similarity 100.0%;
Matches 331; Conservative (
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N-PSDB; ADD70153.
11-FEB-2000;
24-FEB-2000;
02-MAR-2000;
15-MAY-2000;
17-MAY-2000;
22-MAY-2000;
23-AUG-2000;
23-AUG-2000;
02-JUN-2000;
01-DEC-2000;
01-DEC-2000;
01-MAR-2001;
01-JUN-2001;
20-JUN-2001;
20-JUN-2001;
09-JUL-2001;
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98US-010880P.
98US-010885P.
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98US-010885P.
29-SEP-1998;
29-SEP-1998;
29-SEP-1998;
30-SEP-1998;
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Hillan KJ;
Watanabe (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated PRO polypeptide, useful for treating cancerous tumors, cardiac insufficiency disorders, wound healing, diabetes mellitus, thalassemias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Gurney AL,
A, Tumas D,
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Best Local Similarity 100.0%; Pred. No. 1e-165;
Matches 331; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                   L, Eaton DL,
Grimaldi JC,
V, Stewart TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; SEQ ID NO 116; 556pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   Baker KP, Botstein D, Desnoyers Gao W, Goddard A, Godowski PJ, Pan J, Paoni NF, Roy MA, Smith Williams PM, Wood WI;
16-APR-1999; 99US-0129674P.
23-JUN-1999; 99US-0144758P.
26-JUL-1999; 99US-0144758P.
26-JUL-1999; 99US-0145698P.
01-SEP-1999; 99WO-US0201111.
15-SEP-1999; 99WO-US0201111.
15-SEP-1999; 99WO-US0201111.
16-DEC-1999; 99WO-US0201111.
11-FEB-2000; 2000WO-US005841.
11-FEB-2000; 2000WO-US0114941.
15-MAR-2000; 2000WO-US0115264.
22-MAY-2000; 2000WO-US0115264.
23-AUG-2000; 2000WO-US0115264.
23-AUG-2000; 2000WO-US0115264.
23-AUG-2000; 2000WO-US0115264.
23-AUG-2000; 2000WO-US0115264.
23-AUG-2000; 2000WO-US0115264.
21-MAR-2001; 2001WO-US03106520.
21-MAR-2001; 2001WO-US011735.
29-JUN-2001; 2001WO-US021735.
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N-PSDB; ADD38274.
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  Human secreted/transmembrane protein PRO1430
                                                  33
                                                EDEEVARRLWAESARLVGLEAPSVREQPLPR
                                                                                                                                  331
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98US-0098723P.
98US-0098749P.
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98US-0100664P.
98US-0100684P.
98US-0100919P.
98US-0100919P.
98US-0100919P.
                                                                                                                                  standard; protein;
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ADD3923
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Human; secreted protein; transmembrane protein; PRO; tumour; immune response; cardiac insufficiency disorder; calcium flux; umbilical vein endothelial cell; bone disorder; cartilage disorder; arthritis; wound healing; diabetes; skeletal muscle cells; obesity; Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease; dermatitis; herpetiformis; Crohn's disease; thalassaemia.
                                                                                                                                                                                        RGGNIILACRDMEKCBAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVDI
                                                                                                           LINNAGVMRCPHWTTEDGFEMQFGVNHLGHFLLTNLLLDKLKASAPSRIINLSSLAHVAG
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98US-0098723P.
98US-0098723P.
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Hillan KJ;
Watanabe C
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23 - UUL - 1999;

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25 - MAX - 2000;

26 - UUL - 1999;

27 - DEC - 1999;

28 - OCT - 1999;

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20-UUN-2001;
20-UUN-2001;
29-UUN-2001; (GETH 

Fong S; Hillan KJ; Watanabe ż Ferrara N, Gurney AL, A, Tumas D, i, Eaton DL, Grimaldi JC, ( /, Stewart TA 다. 스타. D, Desnoyers I Godowski PJ, C Roy MA, Smith Roy WI; P, Botstein | Goddard A, (Paoni NF, Res PM, Wood W. WPI; 2003-765477/72 N-PSDB; ADD38753. Williams X D 3 Baker þ Gao ä

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PR01773 PRO1018, E tumors, PRO444 PRO1560, PR such as P treating polypeptide useful for New isolated PRO PRO1246, PRO1246

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            Claim
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PRO1773 cardiac

New isolated PRO polypeptides such as PRO1560, PRO444, PRO1018, PRO1244, PRO1244, PRO1246, are useful for treating cancerous tumors and insufficiency disorders.

Claim 12; SEQ ID NO 116; 550pp; English

Fong S; Hillan KJ; Watanabe C

Ferrara N, Gurney AL, A, Tumas D,

Baker KP, Botstein D, Desnoyers L, Eaton DL, Gao W, Goddard A, Godowski PJ, Grimaldi JC, GPan J, Paoni NF, Roy MA, Smith V, Stewart TA, Williams PM, Wood WI;

WPI; 2003-755104/71 N-PSDB; ADD40184.

GENENTECH INC

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Matches 331; Conservative 0; Mismatches 0;
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Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Cremamalia; Eutheria; Primates; Cremamalia; Eutheria; Primates; Cremamalia; Eutheria; Primates; Cremates; Cremamalia; Eutheria; Primates; Cremates; Cremamalia; Eutheria; Primates; Cremates; Cremates
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the EMBL/GenBank/DDBJ databases. TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES

Euteleostomi; Homo.

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Created) Last sequence update) Last annotation update)

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REMINEACO196006; PubMed=10731132;

RA Addans N.D., Celliker S.E., Holf R.A., Evans C.A., Goccayme J.D.,
RA Addans N.D., Celliker S.E., Holf R.A., Hoskins R.A., Galle R.F.,
RA Addans N.D., Celliker S.E., Holf P.W., Hoskins R.A., Galle R.F.,
RA Garoge R.A., Lewis S.E., Randards S. Ambburner W., Handerson S.N.,
Sutron G.G., Worthman J.R., Yandell N.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barndon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayrakarold L., Baslewin D.
RA Ballew R.M., Basu A., Baxendale J., Bayrakarold L., Basley E.M.,
RA Beeson K.Y., Borson B.P., Barndar D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Buller H., Cadisu E., Center A., Chandra I.,
Ra Burtis K.C., Busam D.A., Buller H., Cadisu E., Center A., Chandra I.,
Ra Burtis K.C., Busam D.A., Buller H., Cadisu E., Center A., Chandra I.,
RA Cherry J.M., Cavilelian A.E., Davenport L.B., Davise P.,
RA Cherry J.M., Cavilelian A.E., Gars W., Dudy A.D., Dew II., Dietz S.M.,
Rodes N., Dealcher A., Howland T.G., Mays A.D., Dew II., Dietz S.M.,
Rodes C., Gabrellian A.E., Garrell J.H., Gu Z., Gunn P., Harrisa M.,
Ralush R., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Kethmison J.A.,
Razis D. Houston K.A., Howland T.G., Meis M.P., Morber W. L.,
A Kimmel B.E., Rodra C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Leviteky A.A., Li J., Li Y., Hernandez J., Morris G., Morris G., Morshimm R.,
Raken D., M., Muyhy B., Murphy L., Muzny D.M., Natson D.L.,
Rount S.M., Moy M., Muyphy B., Murphy L., Muzny D.M., Natson D.L.,
A Reinert K., Reington K.A., Nixon K., Nusskern D.R., Pacle D. J.,
Reinert K., Reington K.A., Mixon K., Nusskern D.R., Pacle D. S.,
Reinert K., Reington K.A., Mixon K., Nusskern D.R., Pacle D. J.,
Rades R., Tector C., Turner R., Venter B., Spred B.,
Rades R., Tector C., Turner R., Venter B., Spred B.,
Rades R., Zaveri J.S., Zhan M., Zhou K., Stang S., Zhu X., Smith H.O.,
Rades R., Myserman D.A., Weiler C., We D., Yen S.,
Rades
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STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
Champe M., Chavez C., Borsett V., Dresnek D., Farfan D., Liao G.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.,
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comorpha;
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1 (MAY-2002) to the EMBL/GenBank/DDBJ databases
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
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01-OCT-2002 (TrEMBLrel. 2:
01-JUN-2003 (TrEMBLrel. 2:
LP06328p (CG2070-PA).
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Admen M.D., Celniker S.E., Holt R.A. Evans C.A., Gocayne J.D.,

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Admen M.D., Celniker S.E., Holt R.A. Evans C.A., Gocayne J.D.,

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Admen M.D., Celniker S.E., Holt R.A. Evans C.A., Gocayne J.D.,

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Admentides P.G., Scherer S.E., Lip Pw., Hoskins R.A., Galle R.F.,

RA

Recorge R.A. Lewis S.E. R. Anderson S.A. Amburner M., Henderson S.M.,

Burdon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Feliffer B.D.,

RA Ballew R.M. Jean A. Baxendale J., Bayrakar-gollu. L. Beasley E.M.,

Ballew R.M. Jean A. Baxendale J., Bayrakar-gollu. L. Beasley E.M.,

Raballow R.K., Benos P.V. Berman B.P. Blandari D., Bolthakov S.M.,

Becson K.Y., Benos P.V. Berman B.P. Blandari D., Bolthakov S.M.,

Raberin J.M., Cauday S., Dahlke C., Davengort L.B., Davise P.,

RA Cherry J.M., Cauday S., Dahlke C., Davengort L.B., Davise P.,

RA Cherry J.M., Cauday S., Dahlke C., Devengort L.B., Davise P.,

RA Dutbin K.J. Evangelista C.C. Fortan S., Dulkov B.C., Dunn P.,

RA Dutbin D., Houter A.D., Heiman T.J., Herrades S., Plaischmann W.,

RA Hostin D., Houteron K.A., Howland T.J., Hernandez J.R., Houck J.,

Ralali M., Kaluuh P., Karpen G.H., Ke Z., Kannison J.A., Kachdum K.A.,

Jalali M., Kaluuh P., Karpen G.H., Ke Z., Kannison J.A.,

Raisko P., Leik Kodira C.D., Karpen G.H., Ke Z., Kannison J.A., Mosten H.,

Raisko P., Mateli B., McIntosh T.C., McLeod M.P., Sinth T.,

Raiszolo M., Pittuan G.S., Pan S., Polard J., Mosherfi A.,

Raiszolo M., Pittuan G.S., Pan S., Polard J., Mosherfi A.,

Raiszolo M., Pittuan G.S., Pan S., Polard J., Mosteler F., Shen H.,

Raiszolo M., Pittuan G.S., Pan S., Polard J., Mosteler F., Shen H.,

Raiszolo M., Pittuan G.S., Pan S., Polard J., Mosteler F., Shen H.,

Raiszolo M., Pittuan G.S., Pan S., Polard J., Wolker M., Shugski M.P., Shith T.,

Shies E., Stelen-Kadon S., Simpson M., Stupski M.P., Shith T.,

Shies E., Stelen-Kadon S., Simpson M., Stupski M.P., Shith T.,

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FlyBase;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                 th C.D.,
iker S.E.,
A.D.N.J.,
Richter J.,
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O9V4Q3
O9V4Q3;
O9V4Q3;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 24, Last annotation update)
CG2064 protein.
CG2064 OR BCDNA:SD07613.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Neoptera; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                  Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celniker Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D. Harris N.L., Kronmiller B., Marshall B., Millburn G.H., Rich Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.J., Ashburner M., Gelbart W.M., Rubin G.M., Mung
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                                                                                                                                                                    Lewis S.E.;
"Annotation of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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Best Local Similarity 53.5%; Pred. No. 1,2e-56;
Matches 167; Conservative 43; Mismatches 96;
                                                                                                                                                                                                                                                                                                         the EMBL/GenBank/DDBJ
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EMBL; AY102695; AAM27524.1; -.

EMBL; AY102695; AAM27524.1; -.

EMBL; AE003840; AAF59214.2; -.

FlyBase; FBgn0033203; CG2070.

GO; GO:0016491; F:oxidoreductase act.

GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR002198; ADH short.

Pfam; PF00106; adh short; 1.

PRINTS; PR00080; SDRFAMILY.

Oxidoreductase.

SEQUENCE 325 AA; 36297 MW; B85F4
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Celliker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

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Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

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Milliams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

"Sequencing of Drosophila melanogaster genome.";

I Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. SEQUENCE FROM N.A.

Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N. Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; "Annotation of Drosophila melanogaster genome."; Gibbs R.A., Rubin G.M., Venter S.E., OM N.A. Celniker FROM [4] SEQUENCE FROI Adams M.D.,

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SEQUENCE FROM N.A.

STRAIN=Berkeley;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A corge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
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A wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
A Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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01-MAY-2000 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
CG30491 protein (AT09608p).
CG30495 OR CG17986.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygoneryotera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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Best Local Similarity 53.6%; Pred. No. 1.7e-56;
Matches 170; Conservative 44; Mismatches 101;
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                                                                         activity; IEA
EMBL/GenBank/DDBJ
                                        to the EMBL/GenBank/DDBJ
                                       Submitted (SEP-2002) to the EMBL/Gen EMBL; AE003840; AAF59212.3; -.
FlyBase; FBgn0033205; CG2064.
GO; GO:0016491; F:oxidoreductase act GO; GO:008152; P:metabolism; IEA.
InterPro; IPR002198; ADH short.
Pfam; PF00106; adh short; 1.
PRINTS; PR00080; SDRFAMILY.
SEQUENCE 330 AA; 36581 MW; 1D941
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MEDLINE=20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

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de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha
Ephydroidea; Drosophilidae; Drosophila.
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Best Local Similarity 52.2%; Pred. No. 6.96
Matches 164; Conservative 44; Mismatches
HSSP; P50162; 1AE1.
FlyBase; FBgn0050491; CG30491.
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GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
PRINTS; PR00080; SDRFAMILY.
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01-JUN-2003 (TrEMBLrel. 24, Li
CG2065 protein (RH23455p).
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Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy I., Muzny D.M., Nelson D.L.,

Nelson D.R., Nalson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.

Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

He Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";

"The genome sequence of Drosophila melanogaster.";
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
(SDR) FAMILY:
(SDR) FAMILY.
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Harris M.,
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EMBL; AY071710; AAL49332.1; -.
FlyBase; FBgn0033204; CG2065.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR002198; ADH short.
Pfam; PF00106; adh short.
Pfam; PF00106; adh short.
Oxidoreductase.
SEQUENCE 300 AA; 33378 MW; 4FE7A159BD57FACA C
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                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN=CD-1; TISSUE=Testis;

Goto M., Eddy E.M.;

Tubiquitously expressing gene.";

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

Submitted (JUL-1999) to THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES

(SDR) FAMILY.

REMBL; AB030504; BAA82657.1; -.

RGD; MGI:102581; RGh11.

RGD; MGI:102581; Rch11.

RGO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0008152; P:metabolism; IEA.

RO; GO:0008152; P:metabolism; IEA.
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RLWDVSCDLLG
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                                                                    RDHII OR ARSDRI OR UBE-1B.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinz
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Sciurognathi; Muridae; Murin
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Last sequence update)
Last annotation update)
                   Created)
Last sequence update)
Last annotation update)
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Pred. No. 1.6e-50;
51; Mismatches 92;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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Best Local Similarity 50.2%;
Matches 151; Conservative
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113,
24,
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ulus (Mouse)
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O9R1R9;
O1-MAY-2000
O1-MAY-2000
O1-JUN-2003
UBE-1a.
RDH11 OR ARSI
        USKIKB;
01-MAY-2000
01-MAY-2000
01-JUN-2003
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Goto M.,
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MEDLINE=20196006; PubMed=10731132;

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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

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Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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Σ. ω
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
EMBL; AB030503; BAA82656.1; -.
MGD; MGI:102581; Rdh11.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh short.
Pfam; PF00106; adh short.
Oxidoreductase.
SEQUENCE 293 AA; 32442 MW; 1C4FFA9770F0E9D0 CRC64;
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                                                                                                                                                                                                                                                                                                                                          293;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
CG30495-PA.
CG30495 OR CG17986.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                          Length
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Pred. 1
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D D.A.,
Zheng L.,
Smith H.O.,
                                                                 chum K.A.
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Science 287:2185-2195(2000).

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Isam D.A.,
z S.M.,
Farfan D.,
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a D.E.,
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Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome.";
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Pred. No. 2.1e-47;
1; Mismatches 92;
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FlyBase; FBgn0050495; CG30495.

GO; GO:0016491; F:oxidoreductase act
GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR002198; ADH short.

Pfam; PF00106; adh short; 1.

PRINTS; PR00080; SDRFAMILY.
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49.1%;
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BELONGS
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Submitted (MAR-2000)
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Best Local S
Matches 142
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SEQUENCE FROW N.A.

SEQUENCE FROW N.A.

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SEQUENCE FROW N.A.

SEQUENCE S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., in P.W., Hoskins R.A., Galle R.F., Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Worten J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D., Amn K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfaunkoch C., Baldwin D., Beesen K.Y. Benos P.V., Burnan B.P., Bhandari D., Bolshakov S., Beesen K.Y., Benos P.V., Burnan B.P., Bhandari D., Bolshakov S., Beesen M.R., Bouck J., Butler H., Brokstein P., Brottier P., Abvayley S., Dalke C., Davenport L.B., Davies P., Chandra I., Abbayani A., Bayan A., Dang Z., Mays A.D., Dew I., Dietz S.M., de Pablos B., Delcher A., Dang Z., Mays A.D., Dew I., Dietz S.M., Duchin K.J., Evangelista C.C., Ferraz C., Ferriera S., Flatschmann W., Glodek A., Gong F., Gorrell J.H., Guz J., Guan P., Harris N.L., Harrey D., Hamman T.J., Hernandez J.R., Harris M.L., Haurey D., Hamman T.J., Hernandez J.R., Haurey D., Hamman T.J., Hernandez J., Liang Y., Lin X., Mattei B., Modira C.D., Krayitz S., Kuhp D., Lai Z., Liang K.D., Liu X., Mattei B., Molleon H.P., McDeleler P., Shen H., Ablant T.C., McLeod M.P., McDeleler P., Shen H., Ablant T.C., McLeod M.P., McLeleler P., Shen H., Ablant T.C., McLeod M.P., McLeleler P., Shen H., Ablant K.A., Nixon K., Nikosoki M.P., Bull Y., Bangeon M., Stupski M.P., Shith T., Salper E., Spradling A.C., Stupleton M., Strupski M.P., Shith T., Spier E., Spradling A.C., Stupleton M., Strupski M.P., Shith T., Shipson M., Stupski M.P., Shang S., Yang S.,
                                                                                                                                                           IVLETKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTFSSTTLGPIFWLLVKSPEL
                                                                                                                                                                                                                                                                    GGACPSKATIPGKTVIVTGANTGIGKQTALELARRGGNIILACRDMEKCEAAAKDIRGET
                   3 GGKFRKQTDETGKVAIVTGGNTGLGKETVMELARRGATVYMACRNKEKVERARREIVKET
                                                                                LNHHVNARHLDLASLKSIREFAAKIIEEEERVDILINNAGVMRCPHWTTEDGFEMQFGVN
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                  AAOPSTYLAVAEELADVSGKYFDGLKOKAPAPEAEDEEVARRLWAESAR
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Last sequence update)
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01-JUN-2003 (Tr)
CG3842 protein.
CG3842.
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11 Similarity 49.: 142; Conservative

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SEQUENCE FROM N.A.
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Q7U2X4
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lahy S.J.,
ne P.H.,
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    Zheng
Smith
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TISSUE=Kidney;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.
Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.
                                                                                                                                                                                                                                .,
                                                                                                                                                                                                           406;
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Q7T348;
Q7T348;
Q1-367-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprir Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                      260 LVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAPEAEDEEVARRI
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/
                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                   CRC64;
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.8e-45;
es 116;
                                                                                                                                                                                    85CCF99EC52A6D7D
                                                                                                                                                                                                       Query Match
Best Local Similarity 47.4%; Pred. No. 4.86
Matches 148; Conservative 43; Mismatches
                                                                                                                  activity;
                                                                                      HSSP, P14061; 1FDU.
FlyBase; FBGN0029866; CG3842.
GO; GO:0016491; F:oxidoreductase act
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
PRINTS; PR00080; SDRFAMILY.
Oxidoreductase.
SEQUENCE 406 AA; 44889 MW; 85CCI
                                                                 (SDR) FAMILY.
; AE003437; AAF46156.1;
; P14061; 1FDU.
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1765;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                     TISSUE=Kidney;
Strausberg R.;
Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
EMBL; BC053255; AAH53255.1; -.
Hypothetical protein.
SEQUENCE 309 AA; 34060 MW; ECD2A7B24D24F0E2 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    106;
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ed. No. 4.3e-38;
Mismatches 106
                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
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il Similarity 45.2%;
128; Conservative 44
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Q7U2X4;
Q7U2X4;
01-OCT-2003 (TrEMBLrel. 2:
01-OCT-2003 (TrEMBLrel. 2:
01-OCT-2003 (TrEMBLrel. 2:
Probable oxidoreductase ()
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STRAIN=HTE831 / DSM 14371 / JCM 11309;
MEDLINE=22220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Ridge and its unexpected adaptive capabilities to extreme environments.";
Nucleic Acids Res. 30:3927-3935(2002).
EMBL; AP004599; BAC13678.1; -.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR002198; ADH_short.
R Complete proteome.
SEQUENCE 290 AA; 32273 MW; 0E0C1DE2B433C477 CRC64;
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Oceanobacillu:
NCBL_TaxID=182710;
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23, Last sequence update)
24, Last annotation update)
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6C3AA7C5D33B1B28
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Pred. No. 1.2e-36
51; Mismatches 9
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Pred. No. 5e-37
47; Mismatches
                                                                                                                                                                                                                        DB
DB
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                 Tuberculist; Rv0068; -.
GO: GO: 0016491; F: oxidoreductase act
GO; GO: 0008152; P: metabolism; IEA.
InterPro; IPR002198; ADH short.
Pfam; PF00106; adh short; 1.
PRINTS; PR00080; SDRFAMILY.
Oxidoreductase; Complete proteome.
CONFLICT 214 214 V -> L
SEQUENCE 303 AA; 32399 MW; 6C3AA
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Best Local Similarity 41.8%;
Matches 123; Conservative 6
                                                                                                                                                                                                                   Match
Local Similarity 43.9%;
les 133; Conservative
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Q8EQH7;
Q1-MAR-2003 (TrEMBLrel)
01-MAR-2003 (TrEMBLrel)
01-JUN-2003 (TrEMBLrel)
Alcohol dehydrogenase.
OB1722.
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Q8EQH7
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STRAIN=H37Rv;

MEDLINE=98295987; PubMed=9634230;

MEDLINE=98295987; PubMed=9634230;

MEDLINE=98295987; PubMed=9634230;

A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.

Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

B Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Oliver S., Seeger K., Skelton S., Squares S., Squares R.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

Nature 393:537-544(1998).
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YGQAKLANLL
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"Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.
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Mycobacterium tuberculosis.
Bacteria, Actinobacteria; Actinobacteridae, Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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O53613;
O1-JUN-1998 (TrEMBLrel. 06, Created)
O1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
O1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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AE006919; AAK44298.1;
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OSLGI8;

O1-OCT-2000 (TrEMBLrel. 15, Created)

O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)

O1-OCT-2003 (TrEMBLrel. 24, Last annotation update)

O1-JUN-2003 (TrEMBLrel. 24, Last annotation update)

PO009G03.18 protein (P0030H07.1 protein).

PO009G03.18 OR P0030H07.1.

Oryza sativa (Rice).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

NCBI TaxID=4530;
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, Pclone:P0030H07.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/
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STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chr
clone:P0009G03.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ
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EMBL; AP002522; BAB03618.1; -.

EMBL; AP003045; BAB44039.1; -.

Gramene; Q9LGI8; -.

GO; GO:0016491; F:oxidoreductase act
GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR002198; ADH_Short.

Pfam; PF00106; adh_Short; 1.

PRINTS; PR00080; SDRFAMILY.
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1 K		381-931/0 1931, App 10. 667218 INFORMATI INT: RODIS INT: RODIS PERENCE: PPLICATICATICATICATICATICATICATICATICATICAT	ch 1 S 538	20 A 00 A	80 GA 	540 GA 
99 88886 AUN 486 00008 844		LLT 1 19-833-381 teent No. INERAL INF INTLE OF I ILLE REFER URRENT FI PRIOR FILL VUMBER OF SOFTWARE: ORGANISM: FEATURE: NAME/KEY: LOCATION: OTHER INF	Mat Loca es	13 4	4 7	11 5
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APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Retter, Mark
APPLICANT: Retter, Mark
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Bay, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 332
LENGTH: 2507
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Pred. No. 4.1e
0; Mismatches
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US-09-439-313-332
US-09-439-313-332
Sequence 332, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqui
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US-09-724-864-6

JS-quence 6, Application US/09724864

Sequence 6, Application US/09724864

Patent No. 6380362

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Watson, James G.

TITLE OF INVENTION: Polynucleotides and methods for their prince of INVENTION: by the polynucleotides and methods for their prince of INVENTION NUMBER: US/09/724,864

CURRENT FILING DATE: 2000-11-28

CURRENT FILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSEQ for Windows Version 4.0

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16.5%; Score 297.8; DB 4;
Best Local Similarity 80.1%; Pred. No. 6.8e-61;
Matches 366; Conservative 0; Mismatches 82;
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| US-09-352-616A-332 |
| US-09-352-616A-332 |
| Sequence 332, Application US/09352616A |
| Patent No. 6395278 |
| GENERAL INFORMATION: |
| APPLICANT: Dillon, Davin C. |
| APPLICANT: Harlocker, Susan Louise |
| APPLICANT: Harlocker, Susan Louise |
| APPLICANT: Mitcham, Jennifer Lynn |
| APPLICANT: Mitcham, Jennifer Lynn |
| TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS |
| TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR US |
| TITLE OF INVENTION OF PROSTATE CANCER AND METHODS FOR THEIR US |
| TITLE OF INVENTION NUMBER: US/09/352,616A |
| CURRENT FILING DATE: 1999-07-13 |
| NUMBER OF SEQ ID NOS: 472 |
| SOFTWARE: FastSEQ for Windows Version 3.0 |
| SEQ ID NO 332 |
| LENGTH: 2507 |
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RESULT 5
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; Sequence 332, Application US/09232-1.
; Sequence 332, Application US/09232-1.
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR [
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT APPLICATION NUMBER: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 332
LENGTH: 2507
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Sequence 332, Application US/09636215

Sequence 332, Application US/09636215

Betent No. 6620922

GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Fange, Yuqui
APPLICANT: Ralos, Michael D.
APPLICANT: Rater, Michael D.
APPLICANT: Reter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Li, Samuel
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Stolk, John B.
APPLICANT: Stolk, John B.
APPLICANT: Stolk, William
APPLICANT: Stolk, William
APPLICANT: Stolk, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANGER
FILE REFERENCE: 210121.42777C17
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 332
LENGTH: DAND
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Pred. No. 4.1e
0; Mismatches
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APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 332
LENGTH: 2507
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ed. No. 4.1e-49;
Mismatches 412;
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Best Local Similarity 55.3%;
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ORGANISM: Homo sapien
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Sequence 332, Application US/09685166A

Patent No. 6630305

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
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; Sequence 1, Application US/08464400
; Patent No. 5786204
; GENERAL INFORMATION:
    APPLICANT: HE, ET AL.
    TITLE OF INVENTION: Human Prostatic Specific Rec' TITLE OF INVENTION: Human Prostatic Specific Rec' TITLE OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN
    STREET: 6 BECKER FARM ROAD
    CITY: ROSELAND
    STATE: NEW JERSEY
; COUNTRY: USA
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,40
FILING DATE: Concurrently
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
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REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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US-09-688-489-332
i Sequence 332, Application US/09688489
i Patent No. 6664377
i GENERAL INFORMATION:
i APPLICANT: Xu, Jiangchun
i APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR THEIR USE
i TILE OF INVENTION: CANCER AND METHODS FOR THEIR USE
i FILE REFERENCE: 210121.427D2
i CURRENT FILING DATE: 2000-10-13
i NUMBER OF SEQ ID NOS: 338
i SOFTWARE: FastSEQ for Windows Version 3.0
i SEQ ID NO 332
i LENGTH: 2507
i TYPE: DNA
i ORGANISM: HOMO Sapien
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); Mismatches 412;
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TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1086 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
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                                                                                                                                                                         Specific Reductase
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Pred. No. 8.
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                                                                                                                                                                         Human Prostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
1, Application US/08875273A
0. 6106829
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R: 32
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RFECT 5.1
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E: CECCHI, STEWART
6 BECKER FARM ROAD
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TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
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ilarity 55.8%;
Conservative
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY I
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
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                                                                               APPLICANT: HE, ET AL.
TITLE OF INVENTION: Hume
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BY
ADDRESSEE: CECCHI, STI
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SEQUENCE CHARACTERISTICS
LENGTH: 1086 BASE PAIN
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PRIOR APPLICATION DATA
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SYSTEM: N
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Patent No. 6344198

GENERAL INFORMATION:

APPLICANT: HE, ET AL.

TITLE OF INVENTION: Human Prostatic Sp

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSE: HUMAN GENOME SCIENCES, IN

STREET: 9410 KEY WEST AVE

CITY: ROCKVILLE

STATE: MARYLAND

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2
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REFERENCE/DOCKET NUMBER: PF150D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEO ID NO.
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COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,38
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/464,400
FILING DATE: JUN-05-1995
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 41
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FILING DATE: JUI
CLASSIFICATION:
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                                                                                    Score 233.2; DB 4;
Pred. No. 8.7e-46;
); Mismatches 373;
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1086 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA
US-09-123-386-1
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US-09-833-381-933

Sequence 933, Application US/09833381

Patent No. 6672186

GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. 6672186el Nucleic Aci
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR PILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 933
LENGTH: 234
TYPE: DNA
ORGANISM: Homo sapiens
US-09-833-381-933
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Pred. No. 8.7e-46;
0; Mismatches 373;
                                                                                                                                                                                                                                                                                                     BAIN, GILFILLAN & OLSTEIN
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                                                                      Sequence 1, Application PC/TUS9501827A GENERAL INFORMATION:
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
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TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                       CARELLA, BYRNE,
CECCHI, STEWART
BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US
FILING DATE: Concurrently
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 201-994-11:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENGTH: 1086 BASE PAIRS
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il Similarity 55.8%;
498; Conservative
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NAME: FERRARO, GREGORY D
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                      APPLICANT: HE, ET AL.
TITLE OF INVENTION: Huma
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BY
ADDRESSEE: CECCHI, STE
STREET: 6 BECKER FARM
CITY: ROSELAND
STATE: NEW JERSEY
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STRANDEDNESS: SINGLE
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APPLICATION NUMBER:
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ed. No. 5.4e
Mismatches
                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09103840A; Sequence 1, Application US/09103840A; Patent No. 6294328; GENERAL INFORMATION:
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A; CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 2.2e-29;
0; Mismatches 293;
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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t, c or
                                                                                                                                                                                                                                   Sequence 2, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION: APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R.
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LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculos
FEATURE:
OTHER INFORMATION: CDC 1551
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Best Local Similarity 54.7%;
Matches 357; Conservative
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Search completed: June 23, 2004, 14:47:06 Job time : 160 secs

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model **₹** using search, protein OM protein Search time 21 Seconds (without alignments) 1516.162 Million cell 11:04:49 2004, 23, June Run on

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PIR 78:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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sul No	Scor	% Query Match	Lengt		Д	scription
; ; ; ;		. ~	 	0	7084	bable oxidore
8	m		31	~	7082	othetical prot
ጠ		i	30	N	1472	bable oxidore
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ion: E70848		RESULT 1  F70848  probable oxidoreductase - Mycobacterium tuberculosis (strain H37RV)  C;Species: Mycobacterium tuberculosis  C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000  C;Accession: E70848  R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  Nature 393, 537-544, 1998  A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A;Reference number: A70500; MUID:98295987; PMID:9634230
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-303 <COL>
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A;Residues: 1-303 <COL>
A;Cross-references: GB:AL021428; GB:AL123456; NID:g3261514; FIDN:CAA16249.1; PID:g2808 A;Experimental source: strain H37Rv
C;Genetics: A;Gene: Rv0068
C;Genetics: A;Gene: Rv0068
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology <SADH>
F;15-208/Domain: short-chain alcohol dehydrogenase homology <SADH>

ώ Gaps 22; ch 33.4%; Score 566; DB 2; Length 3C l Similarity 43.9%; Pred. No. 1.3e-37; 133; Conservative 47; Mismatches 101; Indels Query Match Best Local S Matches 133

126 34 ATIP---GKTVIVTGANTGIGKOTALELARRGGNIILACRDMEKCEAAAKDIRGETLNHH VNARHLDLASLKSIREFAAKIIEEEERVDILINNAGVMRCPHWTTEDGFEMQFGVNHLGH 67 VELQELDLTSLASVRAAAAQLKSDHQRIDLLINNAGVMYTPRQTTADGFEMQFGTNHLGH 4 a a g ઠે

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                                                                                                                         S.; Hamlin, N.; Holroyd, 1, S.; Squares, S.
              RESULT 2
H70829
hypothetical protein Rv0439c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: H70829
R;Cohle, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon ; Connor, R.; Davies, J.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, S37-544, 1998
R;Connor, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genon A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70829
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-311 <COL>
A;Coss-references: GB:AL021932; GB:AL123456; NID:93261527; PIDN:CAA17396.1; PID:9290
A;Genetics:
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R; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.F. submitted to the EMBL Data Library, January 1998
A; Reference number: Z22831
A; Residues: 1-304 < JAM>
A; Residues: 1-304 < JAM>
A; Residues: 1-304 < JAM>
A; Experimental source: cosmid B1450
C; Genetics:
A; Note: MLCB1450.07
C; Superfamily: ribitol dehydrogenase; short-chain alcohol c; C; Superfamily: ribitol dehydrogenase; short-chain alcohol c
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Pred. No. 4.9e-35;
2; Mismatches 105;
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Local Similarity 43.3%;
nes 132; Conservative
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RESULT 4
S42651
hypothetical protein - rape
C;Species: Brassica napus (rape)
C;Species: Brassica napus (rape)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
A;Coupe, S.A.; Taylor, J.E.; Isaac, P.G.; Roberts, J.A.
A;Reference number: S42651; MUID:94154236; PMID:8111020
A;Cossion: S42651
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-320 <COU>
A;Cross-references: EMBL:X74225; NID:g456719; PIDN:CAB58175.1; PID:g6065752
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology <SADH>
F;34-235/Domain: short-chain alcohol dehydrogenase homology <SADH>
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Best Local Similarity 42.8%; Pred. No. 1.7e-33;
Matches 125; Conservative 50; Mismatches 93; Indels
        Length
                                                                                                  W
Score 531.5; DB 2;
Pred. No. 7.5e-35;
; Mismatches 101;
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Duesterhoeft, A.;
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LLLDKMKSTARESGVQGRIVNLSSIAHTYTYSEGIKFQGIN-DPAGYSERRAYGQSKLSN
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                                                                                                        PIDN:AAC23625.1;
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C; Species: Arabidopsis thaliana (mcuse-ear cress)
C; Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_chang
C; Accession: T48275
R; Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Submitted to the Protein Sequence Database, April 2000
A; Reference number: Z24490
A; Reference number: Z24490
A; Residues: 1-48275
A; Molecule type: DNA
A; Residues: 1-350 < BEV>
A; Cross-references: EMBL: AL162971
A; Experimental source: cultivar Columbia; BAC clone T22P11
C; Genetics:
A; Map position: 5
A; Introns: 40/1; 136/2; 163/1; 214/2; 240/3; 269/1; 284/3
A; Note: T22P11.130
C; Superfamily: ribitol dehydrogenase; short-chain alcohol deh
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A; Reference number: A84420; MUID: 20083487; PMID: 10617197
A; Accession: A84794
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-321 <STO>
A; Cross-references: GB: AE002093; NID: g3236237; PIDN: AAC236
C; Genetics:
A; Gene: At2g37540; F13M22.4
A; Map position: 2
A; Introns: 40/1; 117/2; 144/1; 195/2; 221/3; 250/1; 265/3
C; Superfamily: ribitol dehydrogenase; short-chain alcohol
                                                                                                                                                                                                                                                 Score 497; DB 2; Le
Pred. No. 4.6e-32;
52; Mismatches 97;
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28.8%; Score 487.5; DB 2;
Best Local Similarity 38.2%; Pred. No. 2.9e-31;
Matches 118; Conservative 54; Mismatches 98;
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11 Similarity 40.8%;
119; Conservative 5
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Best Local S
Matches 119
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                           (st
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다.
                           radiodurans
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                                                                                                          J.D.; Dodson,
T.; Zalewski,
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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                                                                                                                                                                                                                                                                                                                 :AAF12130.1;
                                                                   31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSRIINLSSLAHVAGHIDFDDLNWOTRKYNTKAAYCOSKLAIVLFTKELSRRLOGSGVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --HGSTFSSTTLGPIFWLLVKSPELAAQPSTYL
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N;Alternate names: hypothetical protein F13M22.4
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 02-F
C;Accession: T02520; A84794
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Br
Submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome II BAC F13M22 genomic
A;Reference number: Z14677
A;Accession: T02520
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Kesidues: 1-321 <ROUJ
A;Residues: 1-321 <ROUJ
A;Cross-references: EMBL:AC004684; NID:g3236234; PID:g3236237
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S; Rounsley, S.D.; Shen, M.; VanAken, S.E.; Um
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fra
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59;
                                                                                                         E.K.; Peterson, L.; Utterback,
                   oxidoreductase, short-chain dehydrogenase/reductase family - Deinoco C; Species: Deinococcus radiodurans
C; Species: Deinococcus radiodurans
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-1
C; Accession: H75255
R; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A; Title: Genome sequence of the radioresistant bacterium Deinococcus A; Reference number: A75250; MUID:20036896; PMID:10567266
A; Accession: H75255
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-336 < WHI>A; Residues: 1-336 < WHI>A; Residues: 1-336 < WHI>A; Residues: DR2595
A; Experimental source: strain R1
C; Genetics:
A; Genetics:
A; Genetics:
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A; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.3%; Score 513.5; DB 2; larity 37.9%; Pred. No. 2.3e-33; Conservative 41; Mismatches 121;
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| MARRRLPSMTHGNSSQSDRPRIISPLAPRADAAEVVRG-
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135; Conser
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position:
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Best Local S
Matches 135
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: C70863
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70863
A;Accession: C70863
A;Accession: C70863
A;Accession: C70863
A;Residues: 1-317 <COL>
A;Residues: 1-317 <COL>
A;Cross-references: GB:AL021925; GB:AL123456; NID:g2909556; PIDN:CAA17300.1; PID:g290
A;Experimental source: strain H37Rv
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics: A;Genei Rv2263
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology F;15-209/Domain: short-chain alcohol dehydrogenase homology
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                                                                                                        GSPDB:GN00148
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                                                                                                                                                                                                                                                                                                                                  GAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKOTALELARRGGNIILACRDMEKC
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                                                                                                                                                                                alcohol dehydrogenase
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                                                                                                        PIDN: AAK22385.1
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Pred. No. 2.3e-30;
                                                                                                                                                                                                                              Score 485; DB 2; Pred. No. 4.2e-31; 9; Mismatches 130;
                                                                                                                                                                                 dehydrogenase; short-chain
                                                                                                        NID:913421559;
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                                                                                                                                                                                                                                                                                  29;
A; Accession: E87298
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-323 <STO>
A; Cross-references: GB: AE005673; N.
C; Genetics:
A; Gene: CC0398
C; Superfamily: ribitol dehydrogena
                                                                                                                                                                                                                              Query Match
Best Local Similarity 40.1%;
Matches 132; Conservative 29
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Best Local Similarity 37.7%;
Matches 125; Conservative
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E87298
hypothetical protein CC0398 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: E87298
C;Accession: E87298
B;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Haft, D.H.; Kolon
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       i.; Watanabe, A.; Iriguchi
M.; Yasuda, M.; Tabata, S
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09-Dec-2002
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                                   KYNTKAAYCOSKLAIVLFTKELSRRLOGSGV
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                                   B.G.;
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A.; Larbig,
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 04-Mar-2000 C;Accession: T10561
R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16533
A;Accession: T10561
A;Molecule type: DNA
A;Residues: 1-317 <BEV>
A;Residues: 1-317 <BEV>
A;Cross-references: EMBL:AL050399; GSPDB:GN00062; ATSP:F25E4.30
A;Experimental source: cultivar Columbia; BAC clone F25E4
C;Genetics:
A;Gene: ATSP:F25E4.30
A;Map position: 4
A;Introns: 36/1; 113/2; 140/1; 191/2; 217/3; 246/1; 261/3
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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Local Similarity 37.2%; Pred. No. 8.4e-29;
Les 109; Conservative 56; Mismatches 112;
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Pred. No. 2e-28;
7; Mismatches 1
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Best Local Similarity 39.2%;
Matches 121; Conservative 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OSKLANLLFAYELDRRLRAASASVTSVACHPGYAATNLQLRGPQAAGSRLRLLAMRAANA
                                                                                                                                                                                                                                                                                                                                              6-Feb-2001
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                                                                                                                                                                  LINWOTRKYN
                                           ADGFELQFGSNHLGHFALTAHLLPLLRAAQRARVVSLSSLAARRGRIHFDDLQFE-RSYA
                                                                                                       Gaps
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                                                                                    TKAAYCQSKLAIVLFTKELSRRLQ--GSGVTVNALHPGVARTELGRHTGIHGST-
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0
                           EDGFEMOFGVNHLGHFLLTNLLLDKLKASAPSRIINLSSLAHVAGHIDFDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVGQSAEQGAWPLLYAATNPSID--GGEYIGPGGVLNMRGHPERQQPSAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                      A.D.;
                                                                                                                                                                                                                                         probable oxidoreductase [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_cl
C;Accession: D84206
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pa
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Ruthors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.;
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-316 <STO>
A;Genetics:
C;Genetics:
A;Gene: yajol
                                                                                                                                                                                                                                                                                                                  NRC-1
                                                                                                                                                 ---FSSTTLGPIFWLLVKSPELAAOPSTYLAVAEELADVSGKYF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 457.5; DB 2;
Pred. No. 6.4e-29;
43; Mismatches 129;
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C;Species: Arabidopsis thaliana (mouse-ear cress)
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                                                                                                                                                                                                            KAPAPEAEDEEVARRIMAESARLVGLEAPSVR
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Best Local Similarity 38.6%;
Matches 120; Conservative 4:
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AE3195
dehydrogenase Atu5290 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AE3195
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; Rarp, P.; Romero, P.; Zhang, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                W.; Bancroft,
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124
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                                                                                                                                                                                                                                                                                                                                 RESULT 14
T13447
hypothetical protein T19F6.40 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Mar-2000
C;Accession: T13447; T13449
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancr submitted to the Protein Sequence Database, July 1999
A;Reference number: Z17587
A;Accession: T13447
A;Molecule type: DNA
A;Residues: 1-332 <BEV>
A;Cross-references: EMBL:AL109619; GSPDB:GN00062; ATSP:T19F6.40
A;Experimental source: cultivar Columbia; BAC clone T19F6
C;Genetics:
A;Gene: ATSP:T19F6.40
A;Map position: 4
A;Introns: 41/1; 118/2; 145/1; 197/2; 224/3; 254/1; 269/3
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase home
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 SLKSIREFAAKIIEEEERVDILINNAGVMRCPHWTTEDGFEMOFGVNHLGHFLLTNLLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 KL----KASAPSRIINLSSLAH--VAGH-IDFDDLNWOTR-KYNTKAAYCOSKLAIVLF
ARLELADLDLADLASIRACAAGFRQRHARLDLLFNNAGVMFLPLRRTRDGFEMQMGTNHL
                              -VKSPELAAOPSTYLAVAEELADVSGKYFD-----GLKOKAPAP-EAEDEEVARRLW
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 LFTKELSRRLQGSGVTVNAL--HPGVARTELGRHTGIHGSTFSSTTLGPIFWLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
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Best Local Similarity 40.3%; Pred. No. 4.3e-28;
Matches 118; Conservative 47; Mismatches 105; Indels
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Gordon-Kamm,
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordonster, E.W.
A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A; Reference number: AB2577; MUID:21608550; PMID:11743193
A; Accession: AE3195
A; Accession: AE3195
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-301 < KUR>
A; Residues: 1-301 < KUR>
A; Residues: 1-301 < KUR>
A; Experimental source: strain C58 (Dupont)
C; Genetics:
A; Genetics:
C; Genetics:
A; Genetics:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 HHVNARHLDLASLKSIREFAAKIIEEEERVDILINNAGVMRCP-HWTTEDGFEMOFGVNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 SKATIP---GKTVIVTGANTGIGKQTALELARRGGNIILACRDMEKCEAAAKDIRGETLN
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ed. No. 2e-27;
Mismatches 1
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Pred.
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Best Local Similarity 38.2%;
Matches 117; Conservative 55
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us-10-015-393a-116.rsp

# Ltd GenCore version 5.1.6 (c) 1993 - 2004 Compugen

model % Ω - protein search, using OM protein ; Search time 17 Seconds
 (without alignments)
 1013.837 Million cell updates/sec June 23, 2004, 11:03:04 Run on:

US-10-015-393A-116 1695 1 MSRYLLPLSALGTVAGAAVL......ESARLVGLEAPSVREQPLPR 331

score: Title: Perfect so Seguence: 141681 seqs, 52070155 Searched:

residues

0

BLOSUM62 Gapop 10.0 , Gapext

table:

Scoring

141681 hits satisfying chosen parameters: o F Total number

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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## ALIGNMENTS

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STRAIN=C57BL/6J; TISSUE=Diencephalon, and Liver;

MEDLINE=22354683; PubMed=12466851;

MEDLINE=22354683; PubMed=12466851;

MARAIN=E27BL/6J; TISSUE=Diencephalon, and Liver;

MEDLINE=22354683; PubMed=12466851;

MARAIGO I., Osato N., Sato R., Suzuki H., Yamanaka I., Kiyosawa H., Yaqi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Malla B., Dragani T.A., Fletcher C.F., Forrest A., Forest K.S.,

Magalott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Ramachandran S.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Marande K.,

Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

Wilming L.G., Wynshaw-Boris A., Yanagisawa T., Rind Sakaruma T., Rayawa I.,

Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Rukuda S.,

Ayaraki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

Miyazaki A., Yasahiro M., Imotani K., Ishihi Y., Itoh M., Kagawa I.,

A Yanguishi A., Sokai K., Yasaaki D., Shibata K., Shinagawa A.,

Birney E., Harshizaki Y., Itoh M., Waterston R., Lander B.S., Rogers J.,

Miyazaki A., Yangisaki Y., Sasaki D., Shibata K., Shinagawa I.,

Miyaraki Y., Waki Y., Sasaki Y., Sakai K., Ishida K., Shinagawa I.,

Miyaraki A., Yangisaki Y., Sasaki Y., Ishinagawa A.,

Birney E., Hashizaki Y., Sasaki Y., Ishi W., Sakai K., Sakai 
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nita M.,
Y., Wells C.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                        ö
    37;
                                                                         MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATI PGKTVIVTGANT
                                                                                                                                                                                                                             RGGNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIRVFA
                                                                                                                                                     RGGNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFA
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    Length
  DB 1;
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es 1;
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10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Retinol dehydrogenase 13 (EC 1.1.1.-).
  Score 1688; D
Pred. No. 2.8e
0; Mismatches
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Query Match
Best Local Similarity 99.7%;
Matches 330; Conservative
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DHB HUMAN STANDAKL;

C 08TC12; 09NRW0; 09Y391;

T 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Retinol dehydrogenase 11 (EC 1.1.1.-) (Retinal reductase 1) (RalR1)

DE Rostate short-chain dehydrogenase/reductase 1) (Androgen-regulated short-chain dehydrogenase/reductase 1) (HCV core-binding protein DE Short-chain dehydrogenase/reductase 1) (HCV core-binding protein DE HCBP12) (CGI-82).

GN RDH11 OR PSDR1 OR ARSDR1.

GN RDH11 OR PSDR1 OR ARSDR1.

OS Homo sapiens (Human).

Homo sapiens (Human).

Thimates; Catarrhini; Hominidae; Homo.
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                                                                          short-chain dehydrogenases/reductases
   annotation
                                              activity
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                                              (RDH)
                                                                                                                                                                                                                                                                                                                                                          NAD OR NADP (BY SIMILARITY).
BY SIMILARITY.
MISSING (IN REF. 1; BAC28618)
4EBBCE1643C1FECE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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   functional
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                                               dehydrogenase
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Best Local Similarity 83.6%; Pred. No. 2.4e-110;
Matches 280; Conservative 21; Mismatches 29;
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"Analysis of the mouse transcriptome based 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
-!- FUNCTION: Does not exhibit retinol dehy in vitro (By similarity).
-!- SIMILARITY: Belongs to the short-chain
                                                                                                                                                                                                                                 EMBL; AK028434; BAC25950.1; -.
EMBL; AK028434; BAC25950.1; -.
MGD; MGI:1918732; RGh13.
InterPro; IPR002198; ADH short.
Pfam; PF00106; adh short; 1.
PROSITE; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH SHORT; 1.
Oxidoreductase; NADP.
NP BIND 45 51 NAD ACT SITE 200 200 BY SCONFLICT 114 148 MISS
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                                                                                          (SDR) family
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                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain, Muscle, Placenta, and Prostate;

X MEDLINE=2288257; PubMed=12477932,

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

R Klausner R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K.,

Hopkins R.F., Jordan H., Moore T., Mars S.I., Wang J., Heish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wadin T.B., McKernan K.J., Marley M.J., Hulyk S.W.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Marles S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Habey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevoflenko Y., Bolyse R.A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",

I Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[5]

I DENTIFICATION AS A RETINAL REDUCTASE, AND SUBCELLULAR LOCATION.

Kedishvili N.Y., Chumakova O.V., Chetyrkin S.V., Belyaeva O.V.,

Lapshhna E.A., Lin D.W., Matsumura M., Nelson P.S.,

Lapshhna E.A., Lin D.W., Matsumura M., Nelson P.S.,

Edydence that the human gene for prostate short-chain

dehydrogenase/reductase (PSDRI) encodes a novel retinal reductase

(Ralki).",

L. Brill Chem. 277:28999-28915(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length human
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al reductase.
inol. Also
No steroid
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                                                                               Bumgarner
                                                                                                                           highly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 277:28909-28915 (2002).

1- FUNCTION: Exhibits an oxidoreductive catalytic activity town retinoids. Most efficient as an NADPH-dependent retinal reductived. Most efficient as an NADPH-dependent retinal reductions high activity toward 9-cis and all-trans-retinol. Involved in the metabolism of short-chain aldehydes. No steadehydrogenase activity detected.

1- SUBCELLULAR LOCATION: Type II membrane protein (Probable). Associated with endoplasmic reticulum membrane.

2- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;
Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Probable)
                                                                                                                                                                                                                       ÖH.
                                                                                                                                                                                                                                                                                                                                   W.-C.;
                                        TISSUE=Prostate;
MEDLINE=21139101; PubMed=11245473;
Lin B., White J.T., Ferguson C., Wang S., Vessella R., Bum True L.D., Hood L., Nelson P.S.;
"Prostate short-chain dehydrogenase reductase 1 (PSDR1): a of the short-chain steroid dehydrogenase/reductase family expressed in normal and neoplastic prostate epithelium.";
Cancer Res. 61:1611-1618(2001).
                                                                                                                                                                                                                  Li K., Wang L., Cheng J., Zhang L., Lu Y., Liu Y., Duan "Screening of HCV core binding protein from human liver by using yeast two hybrid system.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                 [3]
SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=20272150; PubMed=10810093;
Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin "Identification of novel human genes evolutionarily Caenorhabditis elegans by comparative proteomics."; Genome Res. 10:703-713(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=2;
IsoId=Q8TC12-2; Sequence=VSP_008159;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Predominantly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  me=1;
IsoId=Q8TC12-1; Sequence=Displayed;
                                                                                                                                                                                       FROM N.A. (ISOFORM 1)
                               (ISOFORM
                             FROM N.A.
                                                                                                                                                                                       SEQUENCE FROM
TISSUE=Liver,
Li K., Wang L.
                                                                                                                                                         Cancer Res.
[2]
                                                                                                                                                                                                                    Li K., "Screening"
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cells of prostate, in both basal and luminal secretory cell populations. Expressed at low levels in spleen, thymus, testis, ovary, small intestine, colon, peripherical blood leukocytes, kidney, adrenal gland and fetal liver. Not detected in prostatic fibromuscular stromal cells, endothelial cells, or infiltrating
                                                                                                                                                lymphocytes.
INDUCTION: By androgens, in prostate cancer cells.
PTM: Not glycosylated.
SIMILARITY: Belongs to the short-chain dehydrogenases/reductases (SDR) family.
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NADP (BY SIMILARITY).

BY SIMILARITY.

Missing (in isoform 2).

/FTId=VSP 008159.

S -> F (IN REF. 4; AAH51291).

A -> V (IN REF. 1).

P -> S (IN REF. 1).

P -> S (IN REF. 4; AAH26274).
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EMBL; AF151840; AAD34077.1; -.

EMBL; BC000112; AAH00112.1; -.

EMBL; BC026274; AAH1727.1; -.

EMBL; BC026274; AAH37302.1; -.

EMBL; BC051291; AAH51291.1; -.

EMBL; BC00106; AAH51291.1; -.

EMBL; BC051291; AAH51291.1; -.

EMBL; BC05112; AAH51291.1; -.

EMBL; BC05112; AAH51291.1; -.

EMBL; BC00001; AAH51291.1;
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); Mismatches 8
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TISSUE=Retina,

X SEQUENCE FROM N.A.

TISSUE=Retina,

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Mars S.I., Wang J., Hsieh F.,

Altachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKerman K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Nilalon D.K., Madan A., Young A.C., Sheychenko Y., Boulfard G.G.,

Mhiting M., Madan A., Young A.C., Sheychenko W.,

Blakesley K.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Cheneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=22354683; PubMed=1246685;

MEDLINE=22354683; PubMed=1246685;

A OKazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

A Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Schriml J., Kanapin A., Matsuda H., Baralov S., Beisel K.W.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

A Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

A Kanal A., Kawaji H., Kawasawa Y., Kedairerki R.M., King B.L.,

Konagaya A., Kurochkin I.V., Lev Y., Lenhard B., Lyons P.A.,

A Maglott D.R., Naltais L., Marchionni L., McKenzie L., Miki H.,

Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

A Ravasi T., Reed J.C., Reed D.J., Ramachandran S.,

Sultana R., Takenaka Y., Taylor M.S., Tagacla R.D., Tomitu M.,

Sultana R., Yawane T., Konno H., Nakamura M., Sakazume N., Sato K.,

A Nilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

A Hara A., Hashikawa T., Konno H., Nakamura M., Sakazume N., Sako K.,

A Hara A., Hashikawa T., Konno H., Nakamura M., Sakazume N., Sakai K., Sakai 
                                                                                                                                                                                                                                                                                                                                                                                                                                             Kondo S.,
Kiyosawa H.
, Gojobori
                                                                                                                                                                                                                                                             Craniata; Vertebrata; Eutel
Sciurognathi; Muridae; Muri
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                     RDHC MOUSE STANDARD; PRT; 316 AA. Q8BYK4; Q91WA5; Q9D1Y4; 10~OCT-2003 (Rel. 42, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Retinol dehydrogenase 12 (EC 1.1.1.-).
                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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Natl. Acad. Sci. U.
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K.W., , Cousins K.S.,

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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FUNCTION: Exhibits an oxidoreductive catalytic activity towards retinoids. Most efficient as an NADPH-dependent retinal reductase Displays high activity toward 9-cis and all-trans-retinol. Also involved in the metabolism of short-chain aldehydes. No steroid dehydrogenase activity detected. Might be the key enzyme in the formation of 11-cis-retinal from 11-cis-retinol during regeneration of the cone visual pigments (By similarity). SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
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BY SIMILARITY.

MISSING (IN REF. 2).

H -> D (IN REF. 1; BAB32258)

CF5745B6710A6148 CRC64;
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nes 99;
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6; Mismatches
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EMBL; AK039233; BAC30288.1; -.
EMBL; BC016204; AAH16204.1; -.
MGD; MGI:1925224; RGh12.
InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; FA
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nilarity 48.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22323226; PubMed=12226107;
Matsumura M., Nelson P.S., Palczewski K.;
Haeseleer F., Jang G.-F., Imanishi Y., Driessen C.A.G.G.,
Matsumura M., Nelson P.S., Palczewski K.;
The vertebrate specificity short chain retinol dehydrogenases from
The vertebrate retina.";
J. Biol. Chem. 277:45537-45546(2002).

-!- FUNCTION: Exhibits an oxidoreductive catalytic activity towards
retinoids. Most efficient as an NADPH-dependent retinal reductase.
C. retinoids high activity toward 9-cis and all-trans-retinol. Also involved in the metabolism of short-chain aldehydes. No steroid dehydrogenase activity detected. Might be the key enzyme in the formation of 11-cis-retinal from 11-cis-retinol during
C. -!- TISSUE SPECIFICITY: Widely expressed, mostly in eye, kidney,
Drain, skeletal msucle and stomach.
C. -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
(SDR) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.

TISSUBSEARIN;

MEDLINE=22388257; FubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Kichards S., Worley K.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Cheneration and initial analysis of more than 15,000 full-length human and mouse cDNA sequences ";

Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                Suzuki
                                                                                                                                                                                 Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Isl Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T. Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M. Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori J. Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Si Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AK054835; BAB70811.1; -.
EMBL; BC025724; AAH25724.1; -.
Genew; HGNC:19977; RDH12.
InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; FALSE_NEG.
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                                                                                                                                                                                                                                                                                                                                        COSKLAIVLFTKELSRRLOGSGVTVNALHPGVARTELGRHTGIHGSTFSSTTLGPIFWLL
                                                                                                                                                                   LKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRGGNIILACRDMEKCEAAAK
                                                                                                                                                                                                                           DIRGETLINHHVNARHLDLASLKSIREFAAKIIEEEERVDILINNAGVMRCPHWTTEDGFE
                                                                                                                                                                                                                                                                                                                                                                     -- LCLLWRLFSPF
                                                                                                                                                                                                                                           THLGVNHLGHFLLTYLLLEQLKVSAPARVVNVSSVAHHIGKIPFHDLQ-SEKRYSRGFAY
                                                                                                                                                                                    MQFGVNHLGHFLLTNLLLDKLKASAPSRIINLSSLAHVAGHIDFDDLNWQTRKYNTKAAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RDHB MOUSE.

Q90YF1; Q9D0U5;
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Retinol dehydrogenase 11 (EC 1.1.1.-) (Retinal reductase 1) (RalR1)
Retinol dehydrogenase/reductase 1) (Androgen-regulated short-chain dehydrogenase/reductase 1) (Short-chain aldehydesshort-chain dehydrogenase/reductase 1) (Short-chain aldehydesshort-chain dehydrogenase) (Cell line MC/9.IL4 derived protein 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

TISSUE=Testis;

MEDLINE=22133316; PubMed=12137953;

Moore S., Pritchard C., Lin B., Ferguson C., Nelson P.S.;

"Isolation and characterization of the murine prostate short-chain dehydrogenase/reductase 1 (Psdr1) gene, a new member of the short-chain steroid dehydrogenase/reductase 293:149-160(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Richardson
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TISSUE=Mast cells;
MEDLINE=94289700; PubMed=8018917;
Hara T., Harada N., Mitsui H., Miura T., Ishizaka T., Miyajima "Characterization of cell phenotype by a novel cDNA library subtraction system: expression of CD8a in a mast cell-derived interleukin-4-dependent cell line.";
Blood 84:189-199(1994).
                                                                                                                                    7,
                                                                                                            316;
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                                                                                                            Length
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BY SIMILARITY.

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1; EAOBEBCFF99B67A8 CR
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                                                                                                         Score 737.5; DB 1;
Pred. No. 8.6e-53;
49; Mismatches 92;
                                                                                                                                     Mismatches
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MEDLINE=22803395; PubMed=12807874;
Kasus-Jacobi A., Ou J., Bashmakov Y.K.,
Goldstein J.L., Brown M.S.;
"Characterization of mouse short-chain (SCALD), an enzyme regulated by SREBPS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                      49;
, NADP;
16
200
161
35065 MW;
5%;
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ilarity 50.5%;
Conservative 49
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151; Conser
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                       Oxidoreductase; N
NP BIND 46
ACT SITE 200
CONFLICT 161
SEQUENCE 316 AA
                                                                                                            Query Match
Best Local S
Matches 151
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MEDLINE=22388257; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo.M.F., Casavant T.L., Scheetz T.E.,

B Doak S.S., Ioquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Sodergren E.J., Lu X., Gibbs R.A.,

A Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Richards A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Generation and initial analysis of more than 15,000 full-length human
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-trans-retinal
-chain
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TISSUE SPECIFICITY: Expressed at higher level in liver and testis.
Expressed at lower levels in smooth muscle, thymus, submaxillary
gland and epididiymis. In testis, expression is restricted to
pachytene spermatocytes. Also expressed in four layers of the
                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=CS7BL/61; TISSUE=Embryo;

X MEDLINE-22356483; PubMed=1246681;
A Vikaido I., Coato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Nikaido I., Coato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Nikaido I., Coato N., Saito R., Suzuki H., Schombach C., Gojobori T., Baldarelli R., Hill D.P. Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S., A Blake J.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Garboldi M., Gissi C., Godzik A., Gough J., Anai A., Kawasawa Y., Kedzierski R.M., King B.L., Kanai A., Kawasiu I., Marchionni L., McKenzie L., Miki H., A Kanai A., Kawasiu I., Marchionni L., McKenzie L., Miki H., A Kanai A., Kurochkin I.V., Lee Y., Lehnard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., A Kavasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Schneider C., Semple C.A., Setou M., Shimada K., Schneider C., Semple C.A., Setou M., Shimada K., Schneider C., Semple C.A., Setou M., Shimada K., Schneider C., Wang Y., Waranae Y., Wall S., Yang L., Wallestedt C., Wang Y., Waranae Y., Wallestedt C., Wang Y., Waranae Y., Wallestedt C., Wang Y., Waranae M., Sakarume N., Shinagawa T., Fukuda S., Hara A., Hashizume W., Imotani R., Ishii Y., Itoh M., Waterston R., Lander E.S., Rogers J., Malanae, S., Shinata K., Shinagawa T., Kangua J., Sakai K., Sakai K., Sakai D., Shibata K., Shinagawa T., Ranalysis of the mouse transcriptome based on functional annotation of G., To Conton C., Salanae M., Shinaya S., Shinata M., Shinaya S., Shinata M., Shinaya S., Shinata M., Shinaya S., Shinata 
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Kiyosawa H.,
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similarity)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: Exhibits an oxidoreductive catalytic activiretinoids. Most efficient as an NADPH-dependent all-treductase. Also involved in the metabolism of short-c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Associated with endoplasmic reticulum membrane ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=1 Comment=A number of isoforms are produced;
  0:0-0(2003)
Chem.
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commercial
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                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB035959; BAA88521.1; ALT_FRAME.

REMBL; AR039032; AAK91516.1; -

REMBL; ARV039032; AAK91516.1; -

REMBL; ARV04413; BAB23296.1; -

REMBL; ARV04413; BAB23296.1; -

REMBL; BC018261; AAH18261.1; -

REMBL; BAA; BC18261.1; -

REMBL; BL018261.1; -

REMBL; BC018261.1; -

REMBL; BAA; BC18261.1; -

REMBL; BL018261.1; -

REMBL; BC018261.1; -

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOFGVNHLGHFLLTNLLLDKLKASAPSRIINLSSLAHVAGHIDFDDLNWQTRKYNTKAAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IKTPQEGAQTSLYCALTEGLESLSGSHFSDCQLAWVSYQGRNEIIARRLWDVSCDLLGL
retina, including the outer segment of rods and cones.

PTM: Not glycosylated (By similarity).

SIMILARITY: Belongs to the short-chain dehydrogenases/reductases (SDR) family.

CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDHE HUMAN STANDARD; PRT; 336 AA.

Q9HBH5;
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Retinol dehydrogenase 14 (EC 1.1.1.-) (Alcohol dehydrogenase PAN2)
RDH14 OR PAN2.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
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Pred. No. 3.2e-52;
0; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50,
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Best Local
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cough a collaboration of EMBL outstation - restrictions on its
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                                                                                                                                                                        TISSUE=B-cell;

MEDLINE=22388257; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B Capleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J. Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalsa U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalsa U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION.

MEDLINE=22323226; PubMed=12226107;

A Haeseleer F., Jang G.-F., Imanishi Y., Driessen C.A.G.G.,

Haeseleer F., Jang G.-F., Imanishi Y., Driessen C.A.G.G.,

Haeseleer F., Jang G.-F., Imanishi Y., Driessen C.A.G.G.,

A Haeseleer F., Jang G.-F., Imanishi Y., Driessen C.A.G.G.,

A Haeseleer F., Jang G.-F., Imanishi Y., Driessen C.A.G.G.,

The vertebrate specificity short chain retinol dehydrogenases from

The vertebrate retina.";

J. Biol. Chem. 277:45537-45546(2002).

-!- FUNCTION: Exhibits an oxidoreductive catalytic activity towards

retinoids. Most efficient as an NADPH-dependent retinal reductase.

C.-!- FUNCTION: Exhibits an oxidoreductive catalytic activity towards

retinoids. Most efficient as an NADPH-dependent retinal reductase.

C. -!- FUNCTION: Exhibits an oxidoreductive and all-trans-retinol. No

steroid dehydrogenase activity detected.

C. -!- TISSUE SPECIFICITY: Expressed in brain, kidney, pancreas and

placenta.

C. -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases

C. -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases

C. -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases

C. -!- SIMILARITY: Demily.
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                                                                        TISSUE=Lung;
Brereton P.S., Li K.X., Krozowski Z.S.;
"Pan2, a novel member of the SCAD superfamily.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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NADP (BY SIMILARITY).
BCC17B3CD6B70DED CRC64;
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Pred. No. 8e-52;
44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF237952; AAG12190.1; -.
EMBL; BC009830; AAH09830.1; -.
HSSP; P50162; 1AE1.
Genew; HGNC:19979; RDH14.
InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh short; 1.
PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; FALSE_NEG.
Oxidoreductase; NADP.
ACT_SITE 217 217 BY SIMILARITY
NP_BIND 50 56 NADP (BY SIMI
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                                               FROM N.A
 TaxID=9606
                                                               TISSUE=Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match
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Best Local
Matches 15
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TISSUE FROM N.A.

TISSUE Breast tumor;

WEDINE = 22388257; pubmed = 12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Alausner R.D., Collins F.S., Wagner L., Scheefer C.F., Bhat N.K.,

Alausner R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Diatchenton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.;

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            collaboration
                                                                                                                157
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-1- FUNCTION: Exhibits an oxidoreductive catalytic activity towards retinoids. Most efficient as an NADPH-dependent retinal reductase Displays high activity toward 9-cis and all-trans-retinol. No steroid dehydrogenase activity detected (By similarity).

-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases (SDR) family.
                                                                                                                                                                              YCOSKLAIVLFTKELSRRLOGSGVTVNALHPGVARTELGRHTGIHGSTFSSTTLGPIFWL
                                                                                                                                                                                                                                                                                                                                          EMQFGVNHLGHFLLTNLLLDKLKASAPSRIINLSSLAHVAGHIDFDDLNWQTRKYNTKAA
                                                                                                                                                                                                                                                             ---VRELDLASLRSVRAFCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGF
                                                                           ----GETLNHHVNARHLDLASLKSIREFAAKIIEEEERVDILINNAGVMRCPHWTTEDGF
                                                                                                                                                                                                                                                                                                                     LVKSPELAAQPSTYLAVAEELADVSGKYFDGLKOKAPAPEAEDEEVARRLWAESARLVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Retinol dehydrogenase 14 (EC 1.1.1.-) (Alcohol dehydrogenase PAN2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
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short
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STRAIN=C57BL/6J; TISSUE=Fetal;
Li K.X., Brereton P.S., Obeyesekere V.R., Krozowski Z.S.
"Cloning of the mouse Pan2 cDNA: a novel member of the salcohol dehydrogenase superfamily.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
GKTVIVTGANTGIGKOTALELARRGGNIILACRDMEKCEAAAKDIR
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Q9ERI6;
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For
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between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrictuse by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-silor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Retina;
MEDLINE=22323226; PubMed=12226107;
Haeseleer F., Jang G.-F., Imanishi Y., Driessen C.A.G.G.,
Matsumura M., Nelson P.S., Palczewski K.;
"Dual-substrate specificity short chain retinol dehydrogen;
the vertebrate retina.";
J. Biol. Chem. 277:45537-45546(2002).
-!- FUNCTION: Exhibits an oxidoreductive catalytic activit
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                                                                                                                                                                                                                                                                                                                      GGACPSKATI PGKTVIVTGANTGIGKOTALELARRGGNI ILACRDMEKC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                          BY SIMILARITY.
NADP (BY SIMILARITY).
A05653655E70802D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               substrat
                                                                                                                                                                                                                                                               Score 722.5; DB 1;
Pred. No. 1.5e-51;
19; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDHC BOVIN STANDARD; PRT; 316 AA. P59837; 10-OCT-2003 (Rel. 42, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Retinol dehydrogenase 12 (EC 1.1.1.-) (Double short chain dehydrogenase/reductase 2). RDH12 OR DSSDR2.
                                                                                                                                                                                  ADH_SHORT; FALSE_NEG
                                                                                            EMBL; AF303831; AAG30904.1; -.
EMBL; BC020094; AAH20094.1; -.
MGD; MGI:1920402; 3110030G19Rik.
InterPro; IPR002198; ADH_Short.
Pfam; PF00106; adh_Short; 1.
PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; FALS!
Oxidoreductase; NADP.
ACT_SITE 215 215 BY S:
NP_BIND 51 57 NADP.
SEQUENCE 334 AA; 36366 MW; AO!
                                                                                                                                                                                                                                                                                          49;
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Local Similarity 49.2%;
es 149; Conservative
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  reductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
retinoids. Most efficient as an NADPH-dependent retinal reductase Displays high activity toward 9-cis and all-trans-retinol. Also involved in the metabolism of short-chain aldehydes. No steroid dehydrogenase activity detected. Might be the key enzyme in the formation of 11-cis-retinal from 11-cis-retinol during regeneration of the cone visual pigments (By similarity). TISSUE SPECIFICITY: Expressed in the eyes. SIMILARITY: Belongs to the short-chain dehydrogenases/reductases (SDR) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          precursor
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 316;
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BY SIMILARITY.
2582630B2CA04185 CRC64;
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98;
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Pred. No. 7.1e-51
2; Mismatches 98
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DHSX HUMAN
STANDARD;
PRT; 330 AA.
DHSX HUMAN
Q8N5I4; Q8WUS4; Q96GR8; Q9NTF6;
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Dehydrogenase/reductase SDR family member on (EC 1.1.-.) (DHRSXY).
                                                                                                                                                                                                                                                                                    EMBL; AY115489; AAM51556.1; -.
InterPro; IPR002198; ADH short.
PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH SHORT; FALSE NEG.
Oxidoreductase; NADP; Vision.
NP BIND 46 52 NADP (BY SIN ACT SITE 200 200 BY SIMILARIT SEQUENCE 316 AA; 35171 MW; 2582630B2C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52;
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 48.7%;
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EC 1.1. -.-) (DHRSXY).
DHRSX OR DHRSSX OR CXORF11.
Homo sapiens (Human).
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TISSUE=Teratocarcinoma;
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RLWNVSCELLGI
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DHSX HUMAN
ID DHSX
AC Q8N5I
DT 10-0C
DT 10-0C
DT 10-0C
DE CEC 1
GN DHRSX
OS HOMO
OC EURAR
OC MAMMA
OX NCBI
RN [1]
RP SEQUE
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                                                                                                                      TISSUE=Brain, Duodenum, and Ovary;

X SEQUENCE FROM N.A., AND VARIANT LYS-297.

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XRausner R.D., Collins F.S., Wagner L., Sheafer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ength human
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                                       Urso
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Koehrer K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S.;
Koehrer K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S.;
Koehrer K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

-!- TISSUE SPECIFICITY: Widely expressed.

-!- MISCELLANEOUS: Belongs to the pseudoautosomal region 1 (PAR1 located at the termini of the long and short arms of the X a chromosomes. This region is essential for meiotic pairing an chromosomes. This region of the PAR1 region causes male steringenes in the PAR1 region escape X inactivation.

-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reduct (SDR) family.
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N
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MEDLINE=21588066; PubMed=11731500; Gianfrancesco F., Sanges R., Esposito T., Tempesta S., Rao E., Rappold G., Archidiacono N., Graves J.A.M., Forabosco A., D'Ul "Differential divergence of three human pseudoautosomal genes their mouse homologs: implications for sex chromosome evolutic Genome Res. 11:2095-2100(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMI the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sib.ch).
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CRC64;
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DEHYDROGENASE/REDUCTASE SDR
ON CHROMOSOME X.
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BY SIMILARITY.
E -> K (in dbSNP:12010).
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-> V (IN REF. 2; 99F9EC7BC122911A
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EMBL; BC019696; AAH19696.1; ALT_INIT.
EMBL; BC032340; AAH32340.1; -.
EMBL; AL137300; CAB70685.1; -.
InterPro; IPR002198; ADH_Bhort.
Pfam; PF00106; adh_short; 1.
PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
Oxidoreductase; Signal; Polymorphism.
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36476 MW;
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330 AA;
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PRINTS; PR00080;
PROSITE; PS00061;
Oxidoreductase; S
SIGNAL 1
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Length 330;

; DB 1; 5.2e-36;

532; No. E

Score Pred.

31.4%;

Similarity

Local

Query Best I

Match

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                                                     -VAGAAVLLKDYV---TGGAC-PSKATIPGKTVIVTGANTGIGKQTALE
                                                                                                                                                                                         PLSAARAALRVYAVGAAVILAQLLRRCRGGFLEPVFPPRPDRVAIVTGGTDGIGYSTAKH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Embryo;
MEDLINE=21588066; PubMed=11731500;
Gianfrancesco F., Sanges R., Esposito T., Tempesta S., Rao E.,
Rappold G., Archidiacono N., Graves J.A.M., Forabosco A., D'Urso M.;
Rappold G., Archidiacono N., Graves J.A.M., Forabosco A., D'Urso M.;
"Differential divergence of three human pseudoautosomal genes and
their mouse homologs: implications for sex chromosome evolution.";
Genome Res. 11:2095-2100(2001).
-!- MISCELLANEOUS: Autosomal gene, which is the ortholog of human
DHRSX, located at the termini of the long and short arms of the y
and Y chromosomes.
-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
(SDR) family.
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Murinae; Mus
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   Indels
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Dehydrogenase/reductase SDR family member on chromosome precursor (EC 1.1.-.-) (SCAD family protein) (DHRSXY) (F
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DEHYDROGENASE/REDUCTASE
ON CHROMOSOME X HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
NCBI_TaxID=10090;
   126;
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Oxidoreductase; Signal.
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Sato K., Demura T., Fukuda H.;
"Cloning of photosynthesis-related genes and their expression somatic embryogenesis in carrot.";
Plant Cell Physiol. 38:77-77(1997).
-!- FUNCTION: Phototransformation of protochlorophyllide (Chlide).
-!- CATALYTIC ACTIVITY: Chlorophyllide A + NADP(+) = protochlorophyllide + NADPH.
-!- PATHWAY: Chlorophyll biosynthesis.
-!- SUBCELLULAR LOCATION: Chloroplast.
-!- SUBCELLULAR LOCATION: Chloroplast.
-!- SIMILARITY: Belongs to the short-chain dehydrogenases/red (SDR) family. POR subfamily.
                                                              80;
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                                                                                                                  NNAGVMRCPHWTTEDGFEMOFGVNHLGHFLLTNLLLDKLKASAP----S
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot
campanulids; Apiales; Apiaceae; Apioideae; Scandiceae; Dau
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                                                             Length
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Q9SDT1;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Protochlorophyllide reductase, chloroplast precursor (PCR) (NADPH-protochlorophyllide oxidoreductase) (POR)
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112; Conser
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NCBI_TaxID=4039;
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This SWISS-PROT entry is copyright, It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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X MEDLINE=96197396; PubMed=8616232;

A Li J., Timko M.P.;

I The pc-1 phenotype of Chlamydomonas reinhardtii results from a deletion mutation in the nuclear gene for NADPH:protochlorophyllide coxidoreductase.";

T Plant Mol. Biol. 30:15-37(1996).

I PLANCTION: Phototransformation of protochlorophyllide (Pchlide) to chlorophyllide (Chlide).

I PATHWAY: Chlorophyllide + NADPH.

I PATHWAY: Chlorophyll biosynthesis.

I PATHWAY: Chlorophyll biosynthesis.

I SUBCELLULAR LOCATION: Chloroplast.

I SUBCELLULAR LOCATION: Chloroplast.

I SIMILARITY: Belongs to the short-chain dehydrogenases/reductases (SDR) family. POR subfamily.
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocal
Chlamydomonadaceae; Chlamydomonas.
NCBI_TaxID=3055;
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C817D57FA7CF27D5 CRC64;
                                                                                            Oxidoreductase;
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Protochlorophyllide reductase, chloroplast precursor (PCR) (NADPH-protochlorophyllide oxidoreductase) (POR)
                                                                                                                                      (POTENTIAL)
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|| Similarity 34.4%; Pred. No. 3e-22
|121; Conservative 48; Mismatches |
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InterPro; IPR002198; ADH short.
InterPro; IPR005979; Prochl reduct.
Pfam; PF00106; adh short; 1.
TIGRFAMS; TIGR01289; LPOR; 1.
Photosynthesis; Chlorophyll biosynthesis; Chloroplast; Transit peptide.
TRANSIT 1
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TRAIN=137c / CC-125;
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140 -LHLDLSSLESVRQFVQNFKASGRRLDALVCNAAVYLPTAKEPRFTA-DGFELSVGTNHL
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01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Probable oxidoreductase (EC 1.-.-.).
Streptomyces antibioticus.
Streptomycineae; Actinobacteridae; Actinomycetales
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1890;
the Buropean Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-scor send an email to license@isb-sib.ch).
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314 HVPLFK--TLFPPFQKYITKGYVSEEEAGRRLAAVISDPKLNKSGAYWSW
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between the Swiss Institute of Bioinformatics and the EM
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PROTOCHLOROPHYLLIDE REDUCTASE
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Matches 108; Conservative 54; Mismatches 117; Indels
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PIR; S71468; S71468.
HSSP; P14061; 1FDU.
InterPro; IPR002198; ADH short.
InterPro; IPR005979; Prochl_reduct.
Pfam; PF00106; adh short; 1.
TIGRFAMS; TIGR01289; LPOR; 1.
Photosynthesis; Chlorophyll biosynthesis; Ox Chloroplast; Transit peptide.
TRANSIT 157 CHLOROPLAST (PO
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MEDLINE=93194813; PubMed=8383668;
Yu T.-W., Chen C.W.;
"The unstable melC operon of Streptomyces a with a Tn4811-homologous locus.";
J. Bacteriol. 175:1847-1852(1993).
-:- SIMILARITY: Belongs to the short-chain
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  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=66 / 1326; TRANSPOSON=Tn4811;
MEDLINE=93077460; PubMed=1332944;
Chen C.W., Yu T.-W., Chung H.-M., Chou C.-F.;
Chen C.W., Yu T.-W., Chung H.-M., Chou C.-F.;
"Discovery and characterization of a new transposable element,
Tn4811, in Streptomyces lividans 66.";
J. Bacteriol. 174:7762-7769(1992).
-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
no restrictions content is in
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2.2e-21;
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PIR; A47089; A47089.
InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
PROSITE; PS00061; ADH_SHORT; 1.
Oxidoreductase.
NP_BIND 9 33 NAD
ACT_SITE 165 BY
SEQUENCE 298 AA; 31415 MW; D
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rPro; IPR002198; ADH_short.; PF00106; adh_short; 1.
ITE; PS00061; ADH_SHORT; 1.
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Search completed: June 23, 2004, 11:08:27 Job time : 19 secs

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NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Insert size: 204523; sum-of-contigs
Quality coverage: 6.54 in Q20 bases; agarose-fp
Quality coverage: 7.57 in Q20 bases; sum-of-contigs
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/note="assembly_name:Contig19"
21119. .30399
/note="assembly_name:Contig20"
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/note="assembly_name:Contig21"
41059. .52180
/note="assembly_name:Contig22"
52281. .65275
/note="assembly_name:Contig23"
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/note="assembly_name:Contig16"
2853. .5901
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/note="assembly_name:Contig24"
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/chromosome="19"
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0; Mismatches 1;
                      Best Local Similarity 99.9%;
Matches 967; Conservative
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Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.3.
NOTE: Transposon sequencing failed to verify the number of repeat copies 67315-69359.
NOTE: Shatter libraries failed to resolve dinucleotide repeat region 171590-171722. Unsure number of repeat copies
171590-171722. Forced join 171695.
Location/Qualifiers
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Submitted (07-OCT-1999) Production Sequencing Facility, DOE Jo
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598,
3 (bases 1 to 187064)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (16-AUG-2002) DOE Joint Genome Institute, 2800 Mitch
Drive, Walnut Creek, CA 94598, USA
On Aug 16, 2002 this sequence version replaced gi:15022008.
Draft Sequence Produced by DOE Joint Genome Institute
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
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1.0 Gapext IDENTITY NUC scoring table:

3373863 segs, 2124099041 residues searched:

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1: geneseqn1980s:\*

3: geneseqn2000s:\*

5: geneseqn2001as:\*

6: geneseqn2001bs:\*

7: geneseqn2003as:\*

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9: geneseqn2003as:\*  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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### ALIGNMENTS

om Parison A membrane bound protein; receptor; diagnosis; i, immunoadhesion; pharmaceutical; screening; ss. Human PRO1430 (UNQ736) cDNA seguence SEQ ID NO:115. AAA37054 standard; cDNA; 1808 BP (first entry) Human; PRO polypeptide; metransmembrane; secretion; 08-AUG-2000 RESULT 1

WO200012708-A2

09-MAR-2000.

98US-0098716P.
98US-0098749P.
98US-0098750P.
98US-0098821P.
98US-00998321P.
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AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCF primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention
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DB; AAY99372.
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